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## OM protein - protein search, using sw model

Run on: August 25, 2005, 04:42:01 ; Search time 166 Seconds  
(without alignments)  
135.133 Million cell updates/sec

Title: US-10-721-961-4

Perfect score: 329  
Sequence: 1 YPVRCILPPATGPGKARIIR.....RGNNANPASEQECSSCGGS 58Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	100.0	58	6	ABG71914 Human Kun
2	326	99.1	58	6	ABG71915 Human Kun
3	314	95.4	58	6	ABG71917 Human Kun
4	314	95.4	111	6	ABG71920 Human Kun
5	291	88.4	58	6	ABG71916 Human Kun
6	291	88.4	111	6	ABG71919 Human Kun
7	264	80.2	58	4	ABG60623 Human pro
8	264	80.2	58	6	ABG71912 Human Kun
9	264	80.2	58	6	ADL16831 Human BTL
10	264	80.2	111	6	ABG71918 Human HKI
11	264	80.2	189	4	ABG60634 Human pro
12	264	80.2	189	8	ADL16845 BTL.010 p
13	264	80.2	1235	8	ADOS5146 Protein #
14	264	80.2	1280	6	ABR58408 Human NOV
15	220.5	67.0	51	4	ABG60631 Human pro
16	220.5	67.0	51	8	ADL16839 Human pro
17	208	63.2	109	2	AAK22985 Kunitz ty
18	203	61.7	111	2	AAK22979 Apoptinin
19	202	61.4	109	2	AAK22983 Apoptinin
20	202	61.4	128	2	AAW82770 Bovine bl
21	199	60.5	57	2	AAW47433 Apoptinin
22	198	60.2	141	2	AAK22982 Apoptinin
23	195	59.3	128	2	AAW82765 Bovine bl
24	194	59.0	111	2	AAK22980 Apoptinin
25	194	59.0	128	2	AAW82768 Bovine bl

26	194	59.0	141	2	AAK22988 Apoptinin
27	194	59.0	141	2	AAK22986 Apoptinin
28	193	58.7	56	1	AAW3399 Apoptinin
29	193	58.7	57	2	AAW47436 Apoptinin
30	193	58.7	57	2	AAW47434 Apoptinin
31	193	58.7	57	2	AAW47432 Apoptinin
32	193	58.7	57	2	AAW47435 Apoptinin
33	193	58.7	128	2	AAW82771 Bovine bl
34	193	58.7	128	2	AAW82772 Bovine bl
35	193	58.7	141	2	AAK22981 Apoptinin
36	193	58.7	141	2	AAK22984 Apoptinin
37	192	58.4	58	1	AAW33401 Apoptinin
38	192	58.4	58	2	AAK27373 Bovine pa
39	192	58.4	58	2	AAK47179 BPTI. 3/2
40	192	58.4	58	2	AAK78426 Bovine pa
41	192	58.4	58	2	AAK81885 Mature bo
42	192	58.4	58	2	AAW9147 Apoptinin
43	192	58.4	58	2	AAW64119 Human Kun
44	192	58.4	58	2	AAW66410 Cationic
45	192	58.4	58	2	AAW79983 Bovine pa

## ALIGNMENTS

RESULT 1	ID	ABG71914 standard; protein; 58 AA.
XX	XX	ABG71914;
DT	22-JAN-2003	(first entry)
XX	XX	Human Kunitz protease inhibitor protein HKI-18, mutant #1.
DE	XX	Human Kunitz protease inhibitor protein HKI-18, mutant #1.
XX	XX	Human; protease inhibitor; kunitz; HKI-18; antiinflammatory;
KW	XX	anticoagulant; coagulant; cardiant; CBP; psoriasis; emphysema;
KW	XX	systemic inflammatory response syndrome; acute pancreatitis;
KW	XX	shock syndrome; disseminated intravascular coagulation; mutant;
KW	XX	hyperfibrinolytic haemorrhage; myocardial infarction; mutein;
KW	XX	cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis;
KW	XX	allergy-induced protease release; deep vein thrombosis;
KW	XX	adult respiratory distress syndrome; chronic inflammatory bowel disease.
OS	XX	Homo sapiens.
XX	XX	Synthetic.
EH	XX	Key
FT	FT	Misc-difference 9 Location/Qualifiers
FT	FT	/note= "Wild-type Ser substituted by Pro"
FT	FT	Misc-difference 11 /note= "Wild-type His substituted by Thr"
FT	FT	Misc-difference 13 /note= "Wild-type Ser substituted by Pro"
FT	FT	Misc-difference 15. .19 /note= "Wild-type Ala-Asp-Trp-Ala-Ala substituted by Lys-Ala-Arg-Ile-Ile"
FT	FT	Misc-difference 34 /note= "Wild-type Trp substituted by Val"
FT	FT	Misc-difference 39 /note= "Wild-type His substituted by Arg"
XX	XX	W0200296938-A2.
PN	XX	05-DEC-2002.
PD	XX	31-MAY-2002; 2002WO-DK000372.
XX	XX	31-MAY-2001; 2001DK-00000859.
PR	XX	05-JUL-2001; 2001US-0303180P.
XX	XX	(NOVO ) NOVO NORDISK AS.
PA	XX	

BEST AVAILABLE COPY

PI Jorgensen MU, Bang S, Olsen OH, Petersen LC;  
 DR MPI; 2003-041403/03.  
 XX  
 XX Kunitz-type protease inhibitor used in the treatment of inflammatory  
 PT disorders.  
 PT  
 PS Claim 20; Page 49; 52pp; English.  
 XX  
 XX The invention relates to an isolated polypeptide comprising a 51 amino  
 CC acid sequence being a generic sequence for a Kunitz-type protease  
 CC inhibitor or a variant where the sequence is at least 80% identical to  
 CC the kunitz domain of human kunitz type protease inhibitor HKI-18. Also  
 CC included are an isolated polypeptide obtainable by cultivation of a host  
 CC cell comprising a polynucleotide construct encoding kunitz-type protein  
 CC in an appropriate growth medium under conditions allowing expression of  
 CC the polynucleotide construct and recovering the polypeptide from the  
 CC culture medium, a polynucleotide construct encoding the kunitz-type  
 CC protein and a host cell comprising the polynucleotide construct. The  
 CC kunitz-type protein is used for the preparation of a medicament for the  
 CC treatment of systemic inflammatory response syndrome, acute pancreatitis,  
 CC shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic  
 CC haemorrhage, myocardial infarction, for prevention of blood loss during  
 CC major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,  
 CC allergy-induced protease release, deep vein thrombosis, emphysema,  
 CC rheumatoid arthritis, adult respiratory distress syndrome, chronic  
 CC inflammatory bowel disease, and psoriasis. The present sequence is a  
 CC human HKI-18 mutant sequence  
 CC  
 XX Sequence 58 AA;  
 SQ  
 Query Match 100.0%; Score 329; DB 6; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-31;  
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 YPVRCLLPPTGPKCKARIIRMYFVASVGCCNRFVGGCGGNANNNFASBQECMSSCGGS 58  
 Db 1 YPVRCLLPPTGPKCKARIIRMYFVASVGCCNRFVGGCGGNANNNFASBQECMSSCGGS 58  
 RESULT 2  
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 ID ABG71915 standard; protein; 58 AA.  
 AC  
 XX ABG71915;  
 AC  
 XX  
 DT 22-JAN-2003 (first entry)  
 XX  
 XX Human Kunitz protease inhibitor protein HKI-18, mutant #2.  
 DE  
 XX  
 XX Human; protease inhibitor; kunitz; HKI-18; antiinflammatory;  
 KW anticoagulant; coagulant; cardiac; CBP; psoriasis; emphysema;  
 KW systemic inflammatory response syndrome; acute pancreatitis;  
 KW shock syndrome; disseminated intravascular coagulation; mutant;  
 KW hyperfibrinolytic haemorrhage; myocardial infarction; muten;  
 KW cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis;  
 KW allergy-induced protease release; deep vein thrombosis;  
 KW adult respiratory distress syndrome; chronic inflammatory bowel disease.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH MISC-difference 9  
 FT /note= "Wild-type Ser substituted by Pro"  
 FT MISC-difference 11  
 FT /note= "Wild-type His substituted by Thr"  
 FT MISC-difference 13  
 FT /note= "Wild-type Ser substituted by Pro"  
 FT MISC-difference 15..19  
 FT /note= "Wild-type Ala-Asp-Trip-Ala-Ala substituted by Arg-  
 FT Ala-Arg-Ile-Ile"  
 FT MISC-difference 34

FT /note= "Wild-type Trp substituted by Val"  
 FT MISC-difference 39  
 FT /note= "Wild-type His substituted by Arg"  
 XX  
 XX  
 XX MO200296938-A2.  
 XX  
 XX  
 PD 05-DEC-2002.  
 XX  
 XX  
 XX 31-MAY-2002; 2002WO-DK000372.  
 XX  
 XX 31-MAY-2001; 2001DK-0000859.  
 PR 05-JUL-2001; 2001US-0303180P.  
 XX  
 XX (NOVO ) NOVO NORDISK AS.  
 PA  
 XX  
 XX Jorgensen MU, Bang S, Olsen OH, Petersen LC;  
 DR MPI; 2003-041403/03.  
 XX  
 XX Kunitz-type protease inhibitor used in the treatment of inflammatory  
 PT disorders.  
 PT  
 PS Claim 20; Page 49; 52pp; English.  
 XX  
 XX The invention relates to an isolated polypeptide comprising a 51 amino  
 CC acid sequence being a generic sequence for a kunitz-type protease  
 CC inhibitor or a variant where the sequence is at least 80% identical to  
 CC the kunitz domain of human kunitz type protease inhibitor HKI-18. Also  
 CC included are an isolated polypeptide obtainable by cultivation of a host  
 CC cell comprising a polynucleotide construct encoding kunitz-type protein  
 CC in an appropriate growth medium under conditions allowing expression of  
 CC the polynucleotide construct and recovering the polypeptide from the  
 CC culture medium, a polynucleotide construct encoding the kunitz-type  
 CC protein and a host cell comprising the polynucleotide construct. The  
 CC kunitz-type protein is used for the preparation of a medicament for the  
 CC treatment of systemic inflammatory response syndrome, acute pancreatitis,  
 CC shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic  
 CC haemorrhage, myocardial infarction, for prevention of blood loss during  
 CC major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,  
 CC allergy-induced protease release, deep vein thrombosis, emphysema,  
 CC rheumatoid arthritis, adult respiratory distress syndrome, chronic  
 CC inflammatory bowel disease, and psoriasis. The present sequence is a  
 CC human HKI-18 mutant sequence  
 CC  
 XX Sequence 58 AA;  
 SQ  
 Query Match 99.1%; Score 326; DB 6; Length 58;  
 Best Local Similarity 98.3%; Pred. No. 2.4e-31;  
 Matches 57; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 YPVRCLLPPTGPKCKARIIRMYFVASVGCCNRFVGGCGGNANNNFASBQECMSSCGGS 58  
 Db 1 YPVRCLLPPTGPKCKARIIRMYFVASVGCCNRFVGGCGGNANNNFASBQECMSSCGGS 58  
 RESULT 3  
 ABG71917  
 ID ABG71917 standard; protein; 58 AA.  
 AC  
 XX ABG71917;  
 AC  
 XX  
 DT 22-JAN-2003 (first entry)  
 XX  
 XX Human Kunitz protease inhibitor protein HKI-18, mutant #4.  
 DE  
 XX  
 XX Human; protease inhibitor; kunitz; HKI-18; antiinflammatory;  
 KW anticoagulant; coagulant; cardiac; CBP; psoriasis; emphysema;  
 KW systemic inflammatory response syndrome; acute pancreatitis;  
 KW shock syndrome; disseminated intravascular coagulation; mutant;  
 KW hyperfibrinolytic haemorrhage; myocardial infarction; muten;  
 KW cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis;  
 KW allergy-induced protease release; deep vein thrombosis;  
 KW adult respiratory distress syndrome; chronic inflammatory bowel disease.

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XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key
XX FT MISC-difference 9 Location/Qualifiers
XX FT MISC-difference 11 /note= "Wild-type Ser substituted by Pro"
XX FT MISC-difference 11 /note= "Wild-type His substituted by Thr"
XX FT MISC-difference 13 /note= "Wild-type Ser substituted by Pro"
XX FT MISC-difference 15.17 /note= "Wild-type Ala-Asp-Trp substituted by Lys-Ala-Arg"
XX FT MISC-difference 34 /note= "Wild-type Trp substituted by Val"
XX PN W0200296938-A2.
XX PD 05-DEC-2002.
XX PF 31-MAY-2002; 2002WO-DK000372.
XX PR 31-MAY-2001; 2001DK-00000859.
XX PR 05-JUL-2001; 2001US-0303180P.
XX PA (NOVO ) NOVO NORDISK AS.
XX PI Jorgensen MU, Bang S, Olsen OH, Petersen LC;
XX DR WPI; 2003-041403/03.
XX PT Kunitz-type protease inhibitor used in the treatment of inflammatory
XX PT disorders.
XX PS Claim 20; Page 49; 52pp; English.
XX XX The invention relates to an isolated polypeptide comprising a 51 amino
XX CC acid sequence being a generic sequence for a Kunitz-type protease
XX CC inhibitor or a variant where the sequence is at least 80% identical to
XX CC the kunitz domain of human kunitz type protease inhibitor HKI-18. Also
XX CC included are an isolated polypeptide obtainable by cultivation of a host
XX CC cell comprising a polynucleotide construct encoding kunitz-type protein
XX CC in an appropriate growth medium under conditions allowing expression of
XX CC the polynucleotide construct and recovering the polypeptide from the
XX CC culture medium, a polynucleotide construct encoding the kunitz-type
XX CC protein and a host cell comprising the polynucleotide construct. The
XX CC kunitz-type protein is used for the preparation of a medicament for the
XX CC treatment of systemic inflammatory response syndrome, acute pancreatitis,
XX CC shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic
XX CC haemorrhage, myocardial infarction, for prevention of blood loss during
XX CC major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,
XX CC allergy-induced protease release, deep vein thrombosis, emphysema,
XX CC rheumatoid arthritis, adult respiratory distress syndrome, chronic
XX CC inflammatory bowel disease, and psoriasis. The present sequence is a
XX CC human HKI-18 mutant sequence
XX SQ Sequence 58 AA;
XX
XX Query Match 95.4%; Score 314; DB 6; Length 58;
XX Best Local Similarity 94.8%; Pred. No. 6.6e-30;
XX Matches 55; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 YPVRCILPAPATGPKARIIRYFVASVGCCNRFYGGCGRGNANFPASEQECSSCGSS 58
XX 1 YPVRCILPAPATGPKARIRYFVASVGCCNRFYGGCGRGNANFPASEQECSSCGSS 58
XX
XX RESULT 4
XX ID ABG71920 standard; protein: 111 AA.
XX AC ABG71920;
XX

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DT 22-JAN-2003 (first entry)
XX XX Human 212L-HKI-18-2 fusion protein.
XX DE
XX XX Human; protease inhibitor; kunitz; HKI-18; antiinflammatory; mutant;
XX KM anticoagulant; coagulant; cardiac; CPB; psoriasis; emphysema; mutein;
XX KM systemic inflammatory response syndrome; acute pancreatitis;
XX KM shock syndrome; disseminated intravascular coagulation; yeast;
XX KM hyperfibrinolytic haemorrhage; myocardial infarction; 212L;
XX KM cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis;
XX KM allergy-induced protease release; deep vein thrombosis;
XX KM adult respiratory distress syndrome; chronic inflammatory bowel disease.
XX XX
XX OS Homo sapiens.
XX OS Saccharomyces cerevisiae.
XX OS Synthetic.
XX OS Chimeric.
XX
XX FH Key
XX FT Peptide 1..51 Location/Qualifiers
XX FT /label= 212L_signal_peptide
XX FT /label= 52..53
XX FT /label= KEX2_cleavage_site
XX FT Protein 54..111
XX FT /label= HKI_18
XX FT MISC-difference 62 /note= "Wild-type Ser substituted by Pro"
XX FT MISC-difference 64 /note= "Wild-type His substituted by Thr"
XX FT MISC-difference 68..70 /note= "Wild-type Ala-Asp-Trp substituted by Lys-Ala-Arg"
XX FT /note= "Wild-type Trp substituted by Val"
XX PN W0200296938-A2.
XX PD 05-DEC-2002.
XX PF 31-MAY-2002; 2002WO-DK000372.
XX PR 31-MAY-2001; 2001DK-00000859.
XX PR 05-JUL-2001; 2001US-0303180P.
XX PA (NOVO ) NOVO NORDISK AS.
XX PI Jorgensen MU, Bang S, Olsen OH, Petersen LC;
XX DR WPI; 2003-041403/03.
XX PT Kunitz-type protease inhibitor used in the treatment of inflammatory
XX PT disorders.
XX PS Example 1; Fig 8; 52pp; English.
XX XX The invention relates to an isolated polypeptide comprising a 51 amino
XX CC acid sequence being a generic sequence for a Kunitz-type protease
XX CC inhibitor or a variant where the sequence is at least 80% identical to
XX CC the kunitz domain of human kunitz type protease inhibitor HKI-18. Also
XX CC included are an isolated polypeptide obtainable by cultivation of a host
XX CC cell comprising a polynucleotide construct encoding kunitz-type protein
XX CC in an appropriate growth medium under conditions allowing expression of
XX CC the polynucleotide construct and recovering the polypeptide from the
XX CC culture medium, a polynucleotide construct encoding the kunitz-type
XX CC protein and a host cell comprising the polynucleotide construct. The
XX CC kunitz-type protein is used for the preparation of a medicament for the
XX CC treatment of systemic inflammatory response syndrome, acute pancreatitis,
XX CC shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic
XX CC haemorrhage, myocardial infarction, for prevention of blood loss during
XX CC major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,
XX CC allergy-induced protease release, deep vein thrombosis, emphysema,
XX CC rheumatoid arthritis, adult respiratory distress syndrome, chronic
XX CC inflammatory bowel disease, and psoriasis. The present sequence
XX CC represents a mutant human HKI-18 with a yeast 212L signal peptide and a
XX CC KEX-2 cleavage site, expressed in yeast cells
XX

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Seq	Sequence	111 AA;
Qy	Query Match	95.4%; Score 314; DB 6; Length 111;
Db	Best Local Similarity	94.8%; Pred. No. 1.3e-29;
	Matches	55; Conservative 0; Mismatches 3; Indels 0; Gaps 0
1	YPRCLLPATGCKKRIIRWYFVAVGQCNRFVYGGCGNANNPASDECKSSCGSS	58
54	YPRCLLPATGCKKRIIRWYFVAVGQCNRFVYGGCGNANNPASDECKSSCGSS	111
RESULT 5		
ABG71916	ABG71916 standard; protein; 58 AA.	
XX		
XX	ABG71916;	
XX		
DT	22-JAN-2003 (first entry)	
DE	Human Kunitz protease inhibitor protein HKI-18, mutant #3.	
XX		
KM	Human; protease inhibitor; kunitz; HKI-18; antiinflammatory;	
KM	anticoagulant; coagulant; cardiant; CBP; psoriasis; emphysema;	
KM	systemic inflammatory response syndrome; acute pancreatitis;	
KM	shock syndrome; disseminated intravascular coagulation; mutant;	
KM	hyperfibrinolytic haemorrhage; myocardial infarction; mitein;	
KM	cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis;	
KM	allergy-induced protease release; deep vein thrombosis;	
KM	adult respiratory distress syndrome; chronic inflammatory bowel disease.	
OS	Homo sapiens.	
OS	Synthetic.	
XX		
XX	Key	Location/Qualifiers
FT	Misc-difference 9	
FT	Misc-difference 11	/note= "Wild-type Ser substituted by Pro"
FT	Misc-difference 15..16	/note= "Wild-type His substituted by Thr"
FT	Misc-difference 15..16	/note= "Wild-type Ala-Asp substituted by Lys-Ala"
PN	NO2002029638-A2.	
XX		
XX	05-DEC-2002.	
XX		
XX	31-MAY-2002; 2002MO-DK000372.	
XX		
XX	31-MAY-2001; 2001DK-00000859.	
PR	05-JUL-2001; 2001JUS-0303180P.	
XX		
XX	(NOVO ) NOVO NORDISK AS.	
XX		
PI	Jorgensen MU, Bang S, Olsen OH, Petersen LC;	
XX		
DR	WPI; 2003-041403/03.	
XX		
PT	Kunitz-type protease inhibitor used in the treatment of inflammatory	
PT	disorders.	
XX		
PS	Claim 20; Page 49; 52pp; English.	
XX		
CC	The invention relates to an isolated polypeptide comprising a 51 amino	
CC	acid sequence being a generic sequence for a Kunitz-type protease	
CC	inhibitor or a variant where the sequence is at least 80% identical to	
CC	the kunitz domain of human kunitz-type protease inhibitor HKI-18. Also	
CC	included are an isolated polypeptide construct encoding kunitz-type protein	
CC	in an appropriate growth medium under conditions allowing expression of	
CC	the polynucleotide construct and recovering the polypeptide from the	
CC	culture medium, a polynucleotide construct encoding the kunitz-type	
CC	protein and a host cell comprising the polynucleotide construct. The	
CC	kunitz-type protein is used for the preparation of a medicament for the	
CC	treatment of systemic inflammatory response syndrome, acute pancreatitis,	

CC	shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic haemorrhage, myocardial infarction, for prevention of blood loss during major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,
CC	allergy-induced procoagulant release, deep vein thrombosis, emphysema,
CC	rheumatoid arthritis, adult respiratory distress syndrome, chronic inflammatory bowel disease, and psoriasis. The present sequence is a human HKI-18 mutant sequence
CC	
XX	Sequence 58 AA;
SQ	
Query Match	89.4%; Score 291; DB 6; Length 56;
Best Local Similarity	89.7%; Pred. No. 3.7e-27;
Matches	52; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Oy	1 YPVACLPATGPKKARIIRWYFVASVGGCNRFFYGGCRGNANNFASEOECSMSSCOGS 58       1 YPVACLPATGSKCAAAARVFVASVGCCNRFYGGCHGNANNFASEOECMSGCCS 58
Dd	
RESULT 6	
ABG71919	
ID	ABG71919 standard; protein; 111 AA.
XX	
AC	ABG71919;
XX	
DT	22-JAN-2003 (first entry)
XX	
DE	Human 212L-HKI-18-1 fusion protein.
KM	Human; protease inhibitor; kunitz; HKI-18; antiinflammatory; mutant; anticoagulant; coagulant; cardiant; CBP; psoriasis; emphysema; mulein; systemic inflammatory response syndrome; acute pancreatitis; shock syndrome; disseminated intravascular coagulation; yeast; hyperfibrinolytic haemorrhage; myocardial infarction; 212L; cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis; allergy-induced procoagulant release; deep vein thrombosis; adult respiratory distress syndrome; chronic inflammatory bowel disease.
KM	
XX	Homo sapiens.
OS	Saccharomyces cerevisiae.
OS	Synthetic.
OS	Chimeric.
XX	
FH	Key Location/Qualifiers
FH	Peptide 1..51
FT	/label= 212L_signal_peptide
FT	Cleavage-site 52..53
FT	/label= KEX2_cleavage_site
FT	Protein 54..111
FT	/label= HKI_18
FT	Misc-difference 62
FT	/note= "Wild-type Ser substituted by Pro"
FT	Misc-difference 64
FT	/note= "Wild-type His substituted by Thr"
FT	Misc-difference 68..69
FT	/note= "Wild-type Ala-Asp substituted by Lys-Ala"
XX	
PX	WO200296938-A2.
PX	
PD	05-DEC-2002.
PF	31-MAY-2002; 2002MO-DK000372.
PR	31-MAY-2001; 2001DK-00000859.
PR	05-JUL-2001; 2001US-0303180P.
PA	(NOVO ) NOVO NORDISK AS.
PI	Jorgensen MU, Bang S, Olsen OH, Petersen LC;
WI	WPI; 2003-041403/03.
XX	
XX	Kunitz-type protease inhibitor used in the treatment of inflammatory

PT disorders.  
 XX  
 PS Example 1; Fig 8; 52pp; English.  
 XX  
 CC The invention relates to an isolated polypeptide comprising a 51 amino  
 CC acid sequence being a generic sequence for a Kunitz-type protease  
 CC inhibitor or a variant where the sequence is at least 80% identical to  
 CC the Kunitz domain of human kunitz type protease inhibitor HKI-18. Also  
 CC included are an isolated polypeptide obtainable by cultivation of a host  
 CC cell comprising a polynucleotide construct encoding kunitz-type protein  
 CC in an appropriate growth medium under conditions allowing expression of  
 CC the polynucleotide construct and recovering the polypeptide from the  
 CC culture medium, a polynucleotide construct encoding the kunitz-type  
 CC protein and a host cell comprising the polynucleotide construct. The  
 CC kunitz-type protein is used for the preparation of a medicament for the  
 CC treatment of systemic inflammatory response syndrome, acute pancreatitis,  
 CC shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic  
 CC hemorrhage, myocardial infarction, for prevention of blood loss during  
 CC major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,  
 CC allergy-induced protease release, deep vein thrombosis, emphysema,  
 CC rheumatoid arthritis, adult respiratory distress syndrome, chronic  
 CC inflammatory bowel disease, and psoriasis. The present sequence  
 CC represents a mutant human HKI-18 with a yeast 212U signal peptide and a  
 CC KEX-2 cleavage site, expressed in yeast cells  
 XX  
 SQ Sequence 111 AA;  
 Query Match 88.4%; Score 291; DB 6; Length 111;  
 Best Local Similarity 89.7%; Pred. No. 7.2e-27;  
 Matches 52; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 YPVRCILPPATGPKARIIRMYFVASVGQCNRFVYGCGRCGNANNFASBOECMSSCGSS 58  
 Db 54 YPVRCILPPATGSKAAARMYFVASVGQCNRFVYGCGRCGNANNFASBOECMSSCGSS 111  
 XX  
 RESULT 7  
 AAB60623  
 ID AAB60623 standard; protein; 58 AA.  
 XX  
 AC AAB60623;  
 XX  
 DT 27-APR-2001 (first entry)  
 XX  
 DE Human protease inhibitor BTL.010 Kunitz domain, SEQ ID NO:1.  
 XX  
 KW Human BTL.010; neutral serine protease inhibitor; elastase inhibitor;  
 KW proteinase-3 inhibitor; Kunitz domain; emphysema;  
 KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;  
 KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;  
 KW platelet activation; blood coagulation; neutrophil activation;  
 KW monocyte activation; angioplasty; inflammatory disease; lung injury;  
 KW vascular injury; nephrotropic; antirheumatic; antiarthritic.  
 XX  
 XX Homo sapiens.  
 OS  
 PN US6180607-B1.  
 XX  
 PD 30-JAN-2001.  
 XX  
 PF 05-AUG-1999; 99US-00369494.  
 XX  
 PR 05-AUG-1999; 99US-00369494.  
 XX  
 PA (DAVI/) DAVIES C.  
 PA (CHEN/) CHEN D.  
 PA (ROCZ/) ROCZNIAK S.  
 XX  
 PI Davies C, Chen D, Roczniaak S;  
 XX  
 DR WPI, 2001-190860/19.  
 DR N-PSDB; AAF59750.  
 XX

PT Novel serine proteinase inhibitor of the Kunitz family, BTL.010 useful  
 PT for treating emphysema, cystic fibrosis, adult respiratory distress  
 PT syndrome, rheumatoid arthritis, organ failure and glomerulonephritis.  
 XX  
 PS Claim 6; Col 9-10; 17pp; English.  
 XX  
 CC The invention relates to a novel human serine protease inhibitor of the  
 CC Kunitz family, BTL.010 (fragments given in AAB60623, AAB60631 and  
 CC AAB60634). The BTL.010 protein is thought to preferentially inhibit  
 CC neutral serine proteases such as elastase and proteinase-3, relative to  
 CC trypsin-like and chymotrypsin-like proteases. A substantial proportion of  
 CC the BTL.010 protein Kunitz domain (AAB60631) was identified via homology  
 CC searching in the Genbank high throughput genomic (HTG) DNA sequence  
 CC database using the Kunitz domain sequences AAB60630, and was confirmed as  
 CC being novel using the Kunitz domain sequences AAB60632, and AAB60633.  
 CC This sequence information was extended to provide a larger region of  
 CC BTL.010 protein sequence data (AAB60634) by identifying an open reading  
 CC frame (ORF) which comprised DNA encoding the BTL.010 Kunitz domain  
 CC fragment in a 399 bp fragment of human genomic DNA (AAF59750),  
 CC corresponding to bases 16016-16414 of Genbank accession number AC004846.  
 CC The entire BTL.010 Kunitz domain sequence (AAB60623) was obtained from  
 CC the BTL.010 ORF-encoded sequence. The BTL.010 protein, and pharmaceutical  
 CC compositions comprising it, may be used for inhibiting protease activity,  
 CC particularly that of leukocyte elastase, in the prevention, treatment or  
 CC amelioration of medical conditions such as emphysema, idiopathic  
 CC pulmonary fibrosis, adult respiratory distress syndrome, cystic fibrosis,  
 CC rheumatoid arthritis, organ failure or glomerulonephritis. BTL.010  
 CC compositions of the invention modulate at least one physiological  
 CC condition such as platelet activation, blood coagulation, neutrophil  
 CC activation, or monocyte activation. BTL.010 is also useful for the  
 CC prophylactic or therapeutic treatment of patients undergoing angioplasty,  
 CC and for the treatment of inflammatory diseases and diseases involving  
 CC lung and vascular injury. The present sequence represents the human  
 CC BTL.010 protease inhibitor Kunitz domain  
 XX  
 SQ Sequence 58 AA;  
 Query Match 80.2%; Score 264; DB 4; Length 58;  
 Best Local Similarity 82.8%; Pred. No. 6.3e-24;  
 Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 Qy 1 YPVRCILPPATGPKARIIRMYFVASVGQCNRFVYGCGRCGNANNFASBOECMSSCGSS 58  
 Db 1 YPVRCILPSAHGSCADWAARMYFVASVGQCNRFVYGCGRCGNANNFASBOECMSSCGSS 58  
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 ABG71912  
 ID ABG71912 standard; protein; 58 AA.  
 XX  
 AC ABG71912;  
 XX  
 DT 22-JAN-2003 (first entry)  
 XX  
 DE Human Kunitz protease inhibitor protein HKI-18.  
 XX  
 KW Human; protease inhibitor; kunitz; HKI-18; antiinflammatory;  
 KW anticoagulant; coagulant; cardiac; CPB; psoriasis; emphysema;  
 KW systemic inflammatory response syndrome; acute pancreatitis;  
 KW shock syndrome; disseminated intravascular coagulation;  
 KW hyperfibrinolytic haemorrhage; myocardial infarction;  
 KW cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis;  
 KW allergy-induced protease release; deep vein thrombosis;  
 KW adult respiratory distress syndrome; chronic inflammatory bowel disease.  
 XX  
 OS Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT 5..55  
 FT Domain /label=Kunitz\_domain  
 FT /note="This domain is claimed in claim 18"  
 XX  
 PN WO200296938-A2.

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XX 05-DEC-2002.
PD
XX
XX 31-MAY-2002; 2002WO-DK000372.
PF
XX
XX 31-MAY-2001; 2001DK-00000859.
PR
XX 05-JUL-2001; 2001US-0303180P.
XX
XX (NOVO ) NOVO NORDISK AS.
XX
XX Jorgensen MU, Bang S, Olsen OH, Petersen LC;
PI
XX MPI: 2003-041403/03.
XX
XX N-PSDB; ABS56455.
XX
XX Kunitz-type protease inhibitor used in the treatment of inflammatory
PT disorders.
XX
XX Claim 19; Fig 2; 52pp; English.
XX
XX The invention relates to an isolated polypeptide comprising a 51 amino
CC acid sequence being a generic sequence for a Kunitz-type protease
CC inhibitor or a variant where the sequence is at least 80% identical to
CC the kunitz domain of human kunitz type protease inhibitor HKI-18. Also
CC included are an isolated polypeptide obtainable by cultivation of a host
CC cell comprising a polynucleotide construct encoding kunitz-type protein
CC in an appropriate growth medium under conditions allowing expression of
CC the polynucleotide construct and recovering the polypeptide from the
CC culture medium, a polynucleotide construct encoding the kunitz-type
CC protein and a host cell comprising the polynucleotide construct. The
CC kunitz-type protein is used for the preparation of a medicament for the
CC treatment of systemic inflammatory response syndrome, acute pancreatitis,
CC shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic
CC haemorrhage, myocardial infarction, for prevention of blood loss during
CC major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, emphysema,
CC rheumatoid arthritis, adult respiratory distress syndrome, chronic
CC inflammatory bowel disease, and psoriasis. The present sequence is human
CC HKI-18
XX
XX
XX Sequence 58 AA;
SQ
Query Match 80.2%; Score 264; DB 6; Length 58;
Best Local Similarity 82.8%; Pred. No. 6.3e-24;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY 1 YPVRCILPPATGPCAKRIIRWYFVASVGQCNRFVYGGCGGNANNFASBOECMSSCGGS 58
DB 1 YPVRCILPPAHSGSCADMAARWYFVASVGQCNRFWYGGCGGNANNFASBOECMSSCGGS 58
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ADL16831
ID ADL16831 standard; peptide; 58 AA.
XX
XX ADL16831;
AC
XX 06-MAY-2004 (first entry)
DT
XX
XX Human BTL.010 protein Kunitz domain (KD) peptide.
DE
XX
XX BTL.010 protein; serine proteinase inhibitor. Kunitz domain; emphysema;
XX idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
XX cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
XX inflammatory disease; oxidative burst; platelet activation;
XX blood coagulation; gene therapy; human; KD.
XX
XX Homo sapiens.
OS
XX
XX US6689582-B1.
XX
XX 10-FEB-2004.
XX
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PF 12-MAY-2000; 2000US-00569670.
XX
XX 05-AUG-1999; 99US-00369494.
XX
XX (FARB ) BAYER PHARM CORP.
XX
XX Davies C, Chen D, Rocznik S;
PI
XX MPI: 2004-141424/14.
XX
XX New isolated polynucleotide encoding BTL.010 serine proteinase, useful
PT for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
PT respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
PT glomerulonephritis.
XX
XX Claim 1; SEQ ID NO 1; 17pp; English.
XX
XX The invention relates to BTL.010, a human serine proteinase inhibitor of
CC the Kunitz family and its corresponding nucleic acid sequence. The
CC sequences of the invention are useful for treating diseases, e.g.
CC emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
CC syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
CC glomerulonephritis or inflammatory diseases. The BTL.010 protein is also
CC useful for preventing neutrophil and monocyte activation and formation of
CC active oxygen species during the oxidative burst of stimulated
CC granulocytes. It is also useful for reducing platelet activation and
CC blood coagulation. BTL.010 DNA is useful in gene therapy. The present
CC sequence is human BTL.010 protein Kunitz domain (KD) peptide.
XX
XX
XX Sequence 58 AA;
SQ
Query Match 80.2%; Score 264; DB 8; Length 58;
Best Local Similarity 82.8%; Pred. No. 6.3e-24;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY 1 YPVRCILPPATGPCAKRIIRWYFVASVGQCNRFVYGGCGGNANNFASBOECMSSCGGS 58
DB 1 YPVRCILPSAHSGSCADMAARWYFVASVGQCNRFWYGGCGGNANNFASBOECMSSCGGS 58
RESULT 10
ABG71918
ID ABG71918 standard; protein; 111 AA.
XX
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XX 22-JAN-2003 (first entry)
DT
XX
XX Human HKI-18/212L signal peptide.
DE
XX
XX Human; protease inhibitor; kunitz; HKI-18; antiinflammatory;
XX anticoagulant; coagulant; cardiant; CBP; psoriasis; emphysema;
XX systemic inflammatory response syndrome; acute pancreatitis;
XX shock syndrome; disseminated intravascular coagulation; yeast;
XX hyperfibrinolytic haemorrhage; myocardial infarction; 212L;
XX cardiopulmonary bypass-induced pulmonary injury; rheumatoid arthritis;
XX allergy-induced protease release; deep vein thrombosis;
XX adult respiratory distress syndrome; chronic inflammatory bowel disease.
XX
XX Homo sapiens.
OS
XX
XX Saccharomyces cerevisiae.
OS
XX
XX Synthetic.
OS
XX
XX Chimeric.
XX
XX Key Location/Qualifiers
FT Peptide 1..51
FT Cleavage-site 52..53
FT /label= KEX2_cleavage_site
FT Protein 54..111
XX /label= HKI_18
XX
XX WO200296938-A2.
```

XX 05-DEC-2002.  
 PD 31-MAY-2002; 2002MO-DK000372.  
 XX PF 31-MAY-2002; 2002MO-DK000372.  
 XX PR 31-MAY-2001; 2001DK-00000859.  
 PR 05-JUL-2001; 2001US-0303180P.  
 XX (NOVO ) NOVO NORDISK AS.  
 PA Jorgensen MU, Bang S, Olsen OH, Petersen LC;  
 PI WPI, 2003-041403/03.  
 DR N-PSDB; AAF56479.  
 XX Kunitz-type protease inhibitor used in the treatment of inflammatory  
 PT disorders.  
 XX Example 1; Fig 7; 52pp; English.  
 PS The invention relates to an isolated polypeptide comprising a 51 amino  
 CC acid sequence being a generic sequence for a Kunitz-type protease  
 CC inhibitor or a variant where the sequence is at least 80% identical to  
 CC the Kunitz domain of human Kunitz-type protease inhibitor HKI-18. Also  
 CC included are an isolated polypeptide obtainable by cultivation of a host  
 CC cell comprising a polynucleotide construct encoding kunitz-type protein  
 CC in an appropriate growth medium under conditions allowing expression of  
 CC the polynucleotide construct and recovering the polypeptide from the  
 CC culture medium, a polynucleotide construct encoding the kunitz-type  
 CC protein and a host cell comprising the polynucleotide construct. The  
 CC kunitz-type protein is used for the preparation of a medicament for the  
 CC treatment of systemic inflammatory response syndrome, acute pancreatitis,  
 CC shock syndrome, disseminated intravascular coagulation, hyperfibrinolytic  
 CC haemorrhage, myocardial infarction, for prevention of blood loss during  
 CC major surgery, cardiopulmonary bypass (CPB)-induced pulmonary injury,  
 CC allergy-induced protease release, deep vein thrombosis, emphysema,  
 CC rheumatoid arthritis, adult respiratory distress syndrome, chronic  
 CC inflammatory bowel disease, and psoriasis. The present sequence  
 CC represents human HKI-18 with a yeast 212L signal peptide and a KEX-2  
 CC cleavage site, expressed in yeast cells  
 XX  
 SQ Sequence 111 AA;  
 Query Match 80.2%; Score 264; DB 6; Length 111;  
 Best Local Similarity 82.8%; Pred. No. 1.2e-23;  
 Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 YPVRCILPPATGFCRKRIIRWYFVASVGQCNRFVYGCGGNANNFASBOECMSSCGGS 58  
 DB 54 YPVRCILPSAHGSCADWAAWYFVASVGQCNRFWYGGCHGNANNFASBOECMSSCGGS 111  
 AC AAB60634;  
 XX 27-APR-2002 (first entry)  
 DT Human protease inhibitor BTL.010 ORF protein sequence, SEQ ID NO:15.  
 XX Human BTL.010; neutral serine protease inhibitor; elastase inhibitor;  
 KM proteinase-3 inhibitor; Kunitz domain; emphysema;  
 KM idiopathic pulmonary fibrosis; adult respiratory distress syndrome;  
 KM cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;  
 KM platelet activation; blood coagulation; neutrophil activation;  
 KM monocyte activation; angioplasty; inflammatory disease; lung injury;  
 KM vascular injury; nephrotropic; antirheumatic; antiarthritic.  
 XX Homo sapiens.  
 OS US6180607-B1.  
 XX PN

XX 30-JAN-2001.  
 PD 05-AUG-1999; 99US-00369494.  
 XX PF 05-AUG-1999; 99US-00369494.  
 XX PR 05-AUG-1999; 99US-00369494.  
 XX (DAVI/) DAVIES C.  
 PA (CHEN/) CHEN D.  
 PA (ROCK/) ROCZNIAK S.  
 PI Davies C, Chen D, Rocznik S;  
 XX WPI, 2001-190860/19.  
 DR N-PSDB; AAF59750.  
 XX Novel serine proteinase inhibitor of the Kunitz family, BTL.010 useful  
 PT for treating emphysema, cystic fibrosis, adult respiratory distress  
 PT syndrome, rheumatoid arthritis, organ failure and glomerulonephritis.  
 XX Disclosure; Col 7-8; 17pp; English.  
 PS The invention relates to a novel human serine protease inhibitor of the  
 CC Kunitz family, BTL.010 (fragments given in AAB60623, AAB60631 and  
 CC AAB60634). The BTL.010 protein is thought to preferentially inhibit  
 CC neutral serine proteases such as elastase and proteinase-3, relative to  
 CC trypsin-like and chymotrypsin-like proteases. A substantial proportion of  
 CC the BTL.010 protein Kunitz domain (AAB60631) was identified via homology  
 CC searching in the Genbank high throughput genomic (HTG) DNA sequence  
 CC database using the Kunitz domain sequences AAB60630, and was confirmed as  
 CC being novel using the Kunitz domain sequences AAB60632, and AAB60633.  
 CC This sequence information was extended to provide a larger region of  
 CC BTL.010 protein sequence data (AAB60634) by identifying an open reading  
 CC frame (ORF) which comprised DNA encoding the BTL.010 Kunitz domain  
 CC fragment in a 399 bp fragment of human genomic DNA (AAF59750).  
 CC corresponding to bases 16016-16414 of Genbank accession number AC004846.  
 CC The entire BTL.010 Kunitz domain sequence (AAB60623) was obtained from  
 CC the BTL.010 ORF-encoded sequence. The BTL.010 protein, and pharmaceutical  
 CC compositions comprising it, may be used for inhibiting protease activity,  
 CC particularly that of leukocyte elastase, in the prevention, treatment or  
 CC amelioration of medical conditions such as emphysema, idiopathic  
 CC pulmonary fibrosis, adult respiratory distress syndrome, cystic fibrosis,  
 CC rheumatoid arthritis, organ failure or glomerulonephritis. BTL.010  
 CC compositions of the invention modulate at least one physiological  
 CC condition such as platelet activation, blood coagulation, neutrophil  
 CC activation, or monocyte activation. BTL.010 is also useful for the  
 CC prophylactic or therapeutic treatment of patients undergoing angioplasty,  
 CC and for the treatment of inflammatory diseases and diseases involving  
 CC lung and vascular injury. The present sequence represents a portion of  
 CC the human BTL.010 protease inhibitor  
 XX  
 SQ Sequence 169 AA;  
 Query Match 80.2%; Score 264; DB 4; Length 169;  
 Best Local Similarity 82.8%; Pred. No. 2.1e-23;  
 Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 YPVRCILPPATGFCRKRIIRWYFVASVGQCNRFVYGCGGNANNFASBOECMSSCGGS 58  
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 AC ADL16845;  
 XX 06-MAY-2004 (first entry)  
 DT BTL.010 protein related protein #2.  
 XX BTL.010 protein; serine proteinase inhibitor; Kunitz family; emphysema;  
 DE ADL16845  
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 ID ADL16845;  
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 DE ADL16845  
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 ID ADL16845;  
 XX ADL16845;  
 AC ADL16845;  
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 XX BTL.010 protein; serine proteinase inhibitor; Kunitz family; emphysema;  
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 XX 06-MAY-2004 (first entry)  
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 ID ADL16845;  
 XX ADL16845;  
 AC ADL16845;  
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 ID ADL16845;  
 XX ADL16845;  
 AC ADL16845;  
 XX 06-MAY-2004 (first entry)  
 DT BTL.010 protein related protein #2.  
 XX BTL.010 protein; serine proteinase inhibitor; Kunitz family; emphysema;  
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 XX ADL16845;  
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 XX 06-MAY-2004 (first entry)  
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 XX BTL.010 protein; serine proteinase inhibitor; Kunitz family; emphysema;  
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 XX ADL16845 standard; protein; 169 AA.  
 ID ADL16845;  
 XX ADL16845;  
 AC ADL16845;  
 XX 06-MAY-2004 (first entry)  
 DT BTL.010 protein related protein #2.  
 XX BTL.010 protein; serine proteinase inhibitor; Kunitz family; emphysema;  
 DE ADL16845  
 XX ADL16845 standard; protein; 169 AA.  
 ID ADL16845;  
 XX ADL16845;  
 AC ADL16845;  
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 XX BTL.010 protein; serine proteinase inhibitor; Kunitz family; emphysema;  
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 ID ADL16845;  
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 XX BTL.010 protein; serine proteinase inhibitor; Kunitz family; emphysema;  
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 ID ADL16845;  
 XX ADL16845;  
 AC ADL16845;  
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 XX BTL.010 protein; serine proteinase inhibitor; Kunitz family; emphysema;  
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 AC ADL16845;  
 XX 06-MAY-2004 (first entry)  
 DT BTL.010 protein related protein #2.  
 XX BTL.010 protein; serine proteinase inhibitor; Kunitz family; emphysema;  
 DE ADL16845  
 XX ADL16845 standard; protein; 169 AA.  
 ID ADL16845;  
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 AC ADL16845;  
 XX 06-MAY-2004 (first entry)  
 DT BTL.010 protein related protein #2.  
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 XX ADL16845;  
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 XX ADL16845 standard; protein; 169 AA.  
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 XX ADL16845 standard; protein; 169 AA.  
 ID ADL16845;  
 XX ADL16845;  
 AC ADL16845;  
 XX 06-MAY-2004 (first entry)  
 DT B



KM		idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
KM		cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
KM		inflammatory disease; oxidative burst; platelet activation;
KM		blood coagulation; gene therapy.
XX		
OS		unidentified.
PH	Key	Location/Qualifiers
FT	Domain	10..67
FT		/note = Kunitz domain
PN		US6689582-B1.
PD		10-FEB-2004.
PF		12-MAY-2000; 2000US-00569670.
PR		05-AUG-1999; 99US-00369494.
XX		(FARB ) BAYER PHARM CORP.
PA		Davies C, Chen D, Rocznik S;
P1		WPI, 2004-141424/14.
DR		
XX		New isolated polynucleotide encoding BTL.010 serine proteinase inhibitor of
PT		for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
PT		respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
XX		glomerulonephritis.
PS		Disclosure: SEQ ID NO 15; 17pp; English.
XX		The invention relates to BTL.010, a human serine proteinase inhibitor of
CC		the Kunitz family and its corresponding nucleic acid sequence. The
CC		sequences of the invention are useful for treating diseases, e.g.
CC		emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
CC		syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
CC		glomerulonephritis or inflammatory diseases. The BTL.010 protein is also
CC		useful for preventing neutrophil and monocyte activation and formation of
CC		active oxygen species during the oxidative burst of stimulated
CC		granulocytes. It is also useful for reducing platelet activation and
CC		blood coagulation. BTL.010 DNA is useful in gene therapy. The present
XX		sequence is a BTL.010 protein related protein.
SQ		Sequence 189 AA;
	Query Match	80.2%; Score 264; DB 8; Length 189;
	Best Local Similarity	82.8%; Pred. No. 2.1e-23;
	Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	
QY		1 YPVACLEPPATGPCKARIIRMYFYVAVGQCNRFFVGCGGNANFPASDECMSCGGSS 58
Db		10 YPVACLPLSAHGSCADMVAARYFYVAVSGCNRFRFWGGCHGNANFPASDECMSCGGSS 67
RESULT 13		
ID	AD055146	AD055146 standard; protein; 1235 AA.
XX		
AC	AD055146;	
DT	15-JUL-2004	(first entry)
XX		
DE		Protein #48 with increased gene expression in renal cell carcinoma.
XX		
KM		cytostatic; gene therapy; differential expression; renal cell carcinoma;
KM		clear cell RCC; papillary RCC; chromophobe/oncocytoma RCC;
KM		sarcomatoid RCC; TCC; Wilms' tumor; gene expression; kidney cancer;
KX		diagnostic marker; cancer.
XX		
OS		Homo sapiens.
XX		
PN		WO2004032842-A2.

```
XX      22-APR-2004 .  
XD  
XX PF    06-OCT-2003; 2003WO-USO31476.  
PF XX  
PR     04-OCT-2002; 2002US-0415775P.  
PR XX  
XA      (VAND-) VAN ANDEL INST.  
XA XX  
PI      Teh BT, Takahashi M;  
PI XX  
DR      WPI; 2004-340789/31.  
DR N-PDB; ADO54960.  
DX  
XX      New nucleic acid and polypeptide compositions, useful in the field of  
PT molecular biology and medicine, in particular for gene expression  
PT profiling, identifying diagnostic markers, and treating certain types of  
PT kidney cancer.  
PS  
XS      Example IV; SEQ ID NO 243; 53bp; English.  
XC  
CC The invention relates to novel genes that are differentially expressed in  
CX sub-types of renal cell carcinomas and methods of detecting them using  
CC nucleic acids and probes. The nucleic acid probes hybridize with part or  
CC all of a coding sequence that is overexpressed in clear cell renal cell  
CC carcinoma (CC-RCC), papillary RCC, chromophobe/oncocytoma RCC,  
CC sarcomatoid RCC, TCC, or Wilms' tumors, which overexpression is based on  
CC comparison to a baseline value. The methods and compositions of the  
CC present invention are useful in the field of molecular biology and  
CC medicine, in particular for gene expression profiling of certain types of  
CC kidney cancers, in identifying diagnostic markers, and treating such as  
CC cancer patients. This sequence corresponds to the protein encoded by a  
CC gene with increased expression in CC-RCC.  
CX  
SQ      Sequence 1235 AA:  
  
Query Match          80.2%; Score 264; DB #: Length 1235;  
Best Local Similarity 82.8%; Pred. No. 1,4e+22;  
Matches   48; Conservative    0; Mismatches 10; Indels    0; Gaps    0;  
  
QY           1 YPVACLPAPTGPCKAIRRMVFVASVGQCNRFFVYGCGRGANNNFASEROCMSGCCS 58  
            ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db         688 YPVACLPSAHGSCADMAAAMRVFAVSVCNRRFYGGCHGNANNFASEROCMSCCS 745  
  
RESULT 14  
ABRS6408  
ID       ABRS6408 standard; protein: 1280 AA.  
AX  
AC       ABRS6408;  
AT  
DT       07-JUL-2003 (first entry)  
TX  
DE       Human NOV22a.  
DZ  
KW       Human; NOV; antidiabetic; anorectic; antibacterial; vitruclide;  
KV immunomodulator; cytosaratic; nocotropic; neuroprotective; dyslipidaemia;  
KV antiParkinsonian; anticipemic; gene therapy; metabolic disorder;  
KV diabetes; obesity; infection; cachexia; cancer; Parkinson's disease;  
KM neurodegenerative disorder; Alzheimer's disease; immune disorder;  
KM haematopoietic disorder.  
OS Homo sapiens.  
OX  
PN       WO2003029423-A2.  
PD  
FD       10-APR-2003 .  
FX  
PX       02-OCT-2002; 2002WO-USO31358.  
PY  
FR       02-OCT-2001; 2001US-0326483P.  
FR 05-OCT-2001; 2001US-0327342P.  
FR 09-OCT-2001; 2001US-0327917P.
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PR 09-OCT-2001; 2001US-0328029P.  
PR 09-OCT-2001; 2001US-0328044P.  
PR 09-OCT-2001; 2001US-0328056P.  
PR 12-OCT-2001; 2001US-0328849P.  
PR 15-OCT-2001; 2001US-0329414P.  
PR 17-OCT-2001; 2001US-0330142P.  
PR 22-OCT-2001; 2001US-0341058P.  
PR 24-OCT-2001; 2001US-0339266P.  
PR 24-OCT-2001; 2001US-0343629P.  
PR 29-OCT-2001; 2001US-0349575P.  
PR 01-NOV-2001; 2001US-0346357P.  
PR 12-APR-2002; 2002US-0371972P.  
PR 12-APR-2002; 2002US-0371980P.  
PR 17-APR-2002; 2002US-0373261P.  
PR 19-APR-2002; 2002US-0373805P.  
PR 23-APR-2002; 2002US-0374738P.  
PR 16-MAY-2002; 2002US-0381101P.  
PR 17-MAY-2002; 2002US-0381635P.  
PR 29-MAY-2002; 2002US-0383830P.  
PR 01-OCT-2002; 2002US-00262839.

(CURA-) CURAGEN CORP.

PI Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Catterton E;  
PI Binger SR, Elleman K, Gerlach VL, Gorman L, Guo X, Ji W, R;  
PI Kerkula R, Leach MD, Li L, Miller CE, Paturajan M, Rieger DK;  
PI Rotherberg ME, Shinkels RA, Smitheon G, Spletke KA, Taupier RJ;  
PI Vernet CM, Voss EZ, Zernhosen BD, Zhong M;

DR WPI; 2003-381625/36.  
DR N-PSDB; ACC72120.

PT NOX polypeptides and nucleic acids useful for diagnosing, preventing or  
PT treating NOX-associated disorders, e.g. diabetes, obesity, cancer or  
PT dyslipidemia, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.

PS Claim 1, Page 177; 487pp; English.

XX The present invention relates to novel human NOV proteins and their  
XX coding sequences (ACCT2075-ACCT2181 and ABR58363-ABR58469). The NOV  
XX proteins are useful in manufacturing a medicament for treating a syndrome  
XX associated with a human disease. The NOV proteins and coding sequences  
XX may be used to diagnose, treat or prevent metabolic disorders such as  
XX diabetes or obesity, infectious, cachexia, cancer, neurodegenerative  
XX disorders such as Alzheimer's disease or Parkinson's disease, immune  
XX disorders, haematopoietic disorders and various dyslipidaemias

SQ Sequence 1280 AA;

Query Match 80.2%; Score 264; DB 6; Length 1280;  
Best Local Similarity 82.8%; Pred. No. 1,4e-22;  
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 YPVRCLLPATGPGCKARIIRWYVAVSGQCNRFVYGGCGNNANNFASBQECSSCGS 58  
DB 752 YPVRCLLPATGPGCKARIIRWYVAVSGQCNRFVYGGCGNNANNFASBQECSSCGS 809

RESULT 15  
AAB60631

ID AAB60631 standard; protein; 51 AA.

AC AAB60631;

XX 27-APR-2001 (first entry)

DE Human protease inhibitor BTL.010 Kunitz domain fragment, SEQ ID NO:9.

KW Human BTL.010; neutral serine protease inhibitor; elastase inhibitor;  
KW proteinase-3 inhibitor; Kunitz domain; emphysema;  
KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;  
KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;

KW platelet activation; blood coagulation; neutrophil activation;  
KW monocyte activation; angioplasty; inflammatory disease; lung injury;  
KW vascular injury; nephrotropic; antirheumatic; antiarthritic.

OS Homo sapiens.

PN US6100607-B1.

PD 30-JUN-2001

PF 05-AUG-1999; 99US-00369494.

PR 05-AUG-1999; 99US-00369494.

PA (DAVI/) DAVIES C.

PA (CHEN/) CHEN D.

PA (ROCE/) ROCZNIAK S.

PI Davies C, Chen D, Rocznik S;

DR WPI; 2001-190860/19.

DR N-PSDB; AAF59750.

PT Novel serine proteinase inhibitor of the Kunitz family, BTL.010 useful  
PT for treating emphysema, cystic fibrosis, adult respiratory distress  
PT syndrome, rheumatoid arthritis, organ failure and glomerulonephritis.  
PS Disclosure; Col 5-6; 17pp; English.

XX The invention relates to a novel human serine protease inhibitor of the  
XX Kunitz family, BTL.010 (fragments given in AAB60623, AAB60631 and  
XX AAB60634). The BTL.010 protein is thought to preferentially inhibit  
XX neutral serine proteases such as elastase and proteinase-3, relative to  
XX trypsin-like and chymotrypsin-like proteases. A substantial proportion of  
XX the BTL.010 protein Kunitz domain (AAB60631) was identified via homology  
XX searching in the Genbank high throughput genomic (HTG) DNA sequence  
XX database using the Kunitz domain sequences AAB60630, and AAB60633.  
XX This sequence information was extended to provide a larger region of  
XX BTL.010 protein sequence data (AAB60634) by identifying an open reading  
XX frame (ORF) which comprised DNA encoding the BTL.010 Kunitz domain  
XX fragment in a 399 bp fragment of human genomic DNA (AAF59750), AC004846.  
XX Corresponding to bases 16016-16414 of Genbank accession number AAB60623.  
XX The entire BTL.010 Kunitz domain sequence (AAB60623) was obtained from  
XX CC the BTL.010 ORF-encoded sequence. The BTL.010 protein, and pharmaceuti-  
XX cal compositions comprising it, may be used for inhibiting protease activity,  
XX particularly that of leukocyte elastase, in the prevention, treatment or  
XX amelioration of medical conditions such as emphysema, idiopathic  
XX pulmonary fibrosis, adult respiratory distress syndrome, cystic fibrosis,  
XX rheumatoid arthritis, organ failure or glomerulonephritis. BTL.010  
XX compositions of the invention modulate at least one physiological  
XX condition such as platelet activation, blood coagulation, neutrophil  
XX activation, or monocyte activation. BTL.010 is also useful for the  
XX prophylactic or therapeutic treatment of patients undergoing angioplasty,  
XX and for the treatment of inflammatory diseases and diseases involving  
XX lung and vascular injury. The present sequence represents a substantial  
XX proportion of the human BTL.010 protease inhibitor Kunitz domain

SQ Sequence 51 AA;

Query Match 67.0%; Score 220.5; DB 4; Length 51;  
Best Local Similarity 80.8%; Pred. No. 8.7e-19;  
Matches 42; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 5 CLIPATGPGCKARIIRWYVAVSGQCNRFVYGGCGNNANNFASBQECSSCGS 56  
DB 1 CLIPATGPGCKARIIRWYVAVSGQCNRFVYGGCGNNANNFASBQECSSCGS 51

Search completed: August 25, 2005, 04:52:21  
Job time : 168 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 25, 2005, 04:48:01 ; Search time 16 Seconds  
(without alignments)  
348.786 Million cell updates/sec

Title: US-10-721-961-4

Perfect score: 329  
Sequence: 1 YVRCILPPATGECRKARIIR.....RGNNPFASEQCMSSCQGS 58

Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192	58.4	100	1 TIBO	basic proteinase i
2	190	57.8	59	2 S00371	isoaprotinin G1 -
3	188	57.1	58	2 S10063	serum basic protei
4	184	55.9	60	1 TIBOR	basic protease
5	184	55.9	100	1 TIBOSP	uterine plasmin/tr
6	174	52.9	122	1 A55115	amyloid precursor
7	168	51.1	111	2 S41082	beta-amyloid precu
8	168	51.1	751	2 A49974	amyloid beta (A4)
9	168	51.1	763	2 A49321	amyloid precursor
10	168	51.1	765	2 S42880	venom basic protei
11	164	49.8	61	1 TIVIT1	basic proteinase i
12	163	49.5	57	2 A59204	taicatoxin serine
13	163	49.5	62	2 A44180	basic proteinase i
14	163	49.5	110	1 TITTOR	basic proteinase i
15	161	48.9	249	2 T32060	hypothetical prote
16	159	48.3	61	2 TITHCBP	proteinase inhibit
17	159	48.3	62	2 S07451	hepatocytic growth
18	159	48.3	252	2 JG0185	isoalbin
19	158	48.0	58	1 TITHAK	Alzheimer's diseas
20	158	48.0	76	2 S06678	Alzheimer's diseas
21	158	48.0	76	2 S03607	Alzheimer's diseas
22	158	48.0	484	4 A32761	hypothetical Alzhe
23	158	48.0	770	1 QRHUA4	Alzheimer's diseas
24	158	47.7	76	2 S04855	Alzheimer's diseas
25	157	47.7	100	2 A32282	Alzheimer's diseas
26	156	47.4	2225	2 T26063	hypothetical prote
27	155	47.4	747	2 JH0773	Alzheimer's diseas
28	154	46.8	123	2 A29652	inter-alpha-trypsi
29	152	46.2	265	2 A53390	Kunitz-type protei

30	152	46.2	349	2 S21089	alpha-1-microglobu
31	151	45.9	62	2 S19327	venom basic protei
32	151	45.9	125	1 TITHOB1	alpha-1-microglobu
33	151	45.9	349	2 S35708	alpha-1-microglobu
34	151	45.9	352	1 TIBOB1	alpha-1-microglobu
35	150	45.6	67	1 TIBOC	trypsin inhibitor
36	148	45.0	64	2 S41399	Kunitz-type protei
37	148	45.0	65	1 TIVIVC	venom basic protei
38	148	45.0	235	2 A54951	tissue factor path
39	148	45.0	1558	2 C89114	protein C37C3.6a f
40	148	45.0	2167	2 T34395	hypothetical prote
41	147	44.7	304	1 TITHUGK	tissue factor path
42	145	44.1	352	1 HCHU	alpha-1-microglobu
43	145	44.1	922	2 T23573	hypothetical prote
44	144	43.8	57	1 TITNVC	venom basic protei
45	144	43.8	302	1 TITRCK	tissue factor path

#### ALIGNMENTS

RESULT 1  
TIBO  
basic proteinase inhibitor precursor - bovine  
N:Alternate names: aprotinin; basic pancreatic trypsin inhibitor; BPT; cationic kallikre  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 24-Apr-1984 #sequence revision 22-Jul-1994 #ext change 09-Jul-2004  
C:Accession: S00277; A30333; S10546; S02486; S28197; A90162; A90736; A90927; A346  
R:Creighton, T.E.; Charles, I.G.  
J. Mol. Biol. 194, 11-22, 1987  
A:Title: Sequences of the genes and polypeptide precursors for two bovine protease inhibi  
A:Reference number: S00277; WUID:87283904; PMID:2441071  
A:Accession: S00277  
A:Molecule type: DNA; mRNA  
A:Residues: 1100 <CR2>  
A:Cross-references: UNIPROT:P00974; GB:M20934; GB:X05274; NID:G162767; PIDN:AAD13685.1; I  
R:Creighton, T.E.; Charles, I.G.  
Cold Spring Harb. Symp. Quant. Biol. 52, 511-519, 1987  
A:Title: Biosynthesis, processing, and evolution of bovine pancreatic trypsin inhibitor.  
A:Reference number: A90926; WUID:88295740; PMID:2456884  
A:Accession: A30333  
A:Molecule type: DNA  
A:Residues: 1-100 <CRE>  
A:Cross-references: GB:M20934; GB:X05274; NID:G162767; PIDN:AAD13685.1; PID:G162769  
R:Kingdon, I.B.; Anderson, S.  
Biochem. J. 233, 443-450, 1986  
A:Title: Sequences encoding two trypsin inhibitors occur in strikingly similar genomic er  
A:Reference number: S10546; WUID:86158754; PMID:2420326  
A:Accession: S10546  
A:Molecule type: DNA  
A:Residues: 34-97 <KIN>  
R:Piorretti, E.; Angeletti, M.; Fiorucci, L.; Barra, D.; Bossa, F.; Ascoli, F.  
Biol. Chem. Hoppe-Seyler 369(Suppl.), 37-42, 1988  
A:Title: Aprotinin-like isoinhibitors in bovine organs.  
A:Reference number: S02485; WUID:89076531; PMID:2462435  
A:Accession: S02486  
A:Molecule type: protein  
A:Residues: 36-93 <RIO>  
R:Ilekita, M.; Jone, C.S.; Kamo, M.; Tsugita, A.; Kiukki, K.; Moriya, H.  
Protein Seq. Data Anal. 5, 7-11, 1992  
A:Title: Purification and characterization of the major cationic kallikrein inhibitor in  
A:Reference number: S28197; WUID:93150003; PMID:1283464  
A:Accession: S28197  
A:Molecule type: protein  
A:Residues: 36-93 <IKK>  
R:Kasell, B.; Laskowski, M.  
Biochem. Biophys. Res. Commun. 20, 463-468, 1965  
A:Title: The basic trypsin inhibitor of bovine pancreas. V. The disulfide linkages.  
A:Reference number: A90162; WUID:66083012; PMID:5860161  
A:Contents: annotation; disulfide bonds  
A:Accession: A90162  
A:Molecule type: protein  
A:Residues: 36-93 <RAS>

R.Anderer, F.A. Hornle, S. J. Biol. Chem. 241, 1568-1572, 1966  
A:Title: The disulfide linkages in kallikrein inactivator of bovine lung.  
A:Reference number: A92023; MUID:66171231; PMID:5296424  
A:Contents: annotation; disulfide bonds  
A:Accession: A92023  
A:Molecule type: protein  
A:Residues: 36-93 <AN2>  
R:Chauvet, J., Acher, R. Bull. Soc. Chim. Biol. 49, 985-1000, 1967  
A:Title: La structure covalente d'un inhibiteur polypeptidique de la trypsin (inhibiteur de la trypsin)  
A:Reference number: A90736; MUID:68012003; PMID:6053284  
A:Contents: annotation; disulfide bonds  
A:Accession: A90736  
A:Molecule type: protein  
A:Residues: 36-93 <CHA>  
R.Dlouha, V.; Pospisilova, D.; Meloun, B.; Sorm, F. Collect. Czech. Chem. Commun. 33, 1363-1365, 1968  
A:Title: Sequence of residues 18-20 in pancreatic trypsin inhibitor.  
A:Reference number: A90927  
A:Accession: A90927  
A:Molecule type: protein  
A:Residues: 36-93 <DLO>  
R:Huber, R.; Kukla, D.; Ruhlmann, A.; Epp, O.; Formanek, H. Naturwissenschaften 57, 389-392, 1970  
A:Title: The basic trypsin inhibitor of bovine pancreas. I. Structure analysis and configuration of the active site  
A:Reference number: A93410; MUID:70255230; PMID:5447861  
R:Lewis, R.V.; Ray, P.; Cogull, R.; Kruggel, W. Biochem. Biophys. Res. Commun. 167, 543-547, 1990  
A:Title: Presence of pancreatic trypsin inhibitor in adrenal medullary chromaffin cells  
A:Reference number: A34658; MUID:90211226; PMID:2322242  
A:Accession: A34658  
A:Molecule type: protein  
A:Residues: 36-53, 55-81 <LEW>  
R:Anderson, S.; Kingston, I.B. Proc. Natl. Acad. Sci. U.S.A. 80, 6838-6842, 1983  
A:Title: Isolation of a genomic clone for bovine pancreatic trypsin inhibitor by using a cDNA library  
A:Reference number: A93977; MUID:84070725; PMID:6580617  
A:Accession: A93977  
A:Molecule type: DNA  
A:Residues: 'PSLFNRDPIPA', 34-97, 'GTGGRAEGEGK' <AND>  
A:Cross-references: GB:X03365; GB:R00966; NID:g142; PDB:1G136183  
R:Stekmann, J., Wenzel, H.R.; Schroeder, W.; Tschesche, H. Biol. Chem. Hoppe-Seyler 369, 157-163, 1988  
A:Title: Characterization and sequence determination of six aprotinin homologues from bovine pancreas  
A:Reference number: S00371; MUID:88221840; PMID:2453200  
A:Accession: S10062  
A:Molecule type: protein  
A:Residues: 36-66, 'P', 68-82, 'S', 84-93 <STE>  
A:Experimental source: lung  
A:Note: The authors designated this protein as isoaprotinin 2  
C:Comment: Basic proteinase inhibitor is an intracellular polypeptide found in many tissues  
C:Genetics:  
A:Introns: 34/1; 98/1  
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog  
C:Keywords: serine proteinase inhibitor  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-35/Domain: propeptide #status predicted <PRO>  
F:36-100/Product: basic proteinase inhibitor #status experimental <WAT>  
F:40-90/Domain: animal Kunitz-type proteinase inhibitor homolog <BRI>  
F:40-90, 49-73, 65-86/Disulfide bonds: #status experimental  
F:50/Inhibitory site: Lys (trypsin), chymotrypsin, kallikrein, plasmin #status experimental

RESULT 2  
 S00371  
 Isoaprotinin G1 - bovine hybrid  
 C/Species: Bos primigenius indicus x Bos primigenius taurus (cattle)  
 C/Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
 C/Accession: S00371  
 R/Siekman, J.; Wenzel, H.R.; Schroeder, W.; Tschesche, H.  
 Biol. Chem. Hoppe-Seyler 369, 157-163, 1988  
 A1/Title: Characterization and sequence determination of six aprotinin homologues from bo  
 A/Reference number: S00371; MUID:88221840; PMID:2453200  
 A/Accession: S00371  
 A/Molecule type: Protein  
 A/Residues: 1-59 <SIE>  
 A/Cross-references: UNIPROT:Q7M311  
 C/Keywords: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homology  
 C/Keywords: pyroglutamic acid; serine proteinase inhibitor  
 F16-56/Domains: animal Kunitz-type proteinase inhibitor homology <BPI>  
 F11/Modified site: pyroglutamate carboxylic acid (Gln) #status predicted  
 F116/inhibitory site: Lys (tyrosin) #status predicted

```

Query_Match 57.8%; Score 190; DB 2; Length 59;
Best Local Similarity 56.1%; Pred. No. 2.7e-16;
Matches 32; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Cy      2 PYRCLLPATGPCKARIIRWYFVAVSGCCNRFPYGGCRGNANNFASPEGCMSSCGGS 58
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      3 PDFGLPEPTGCKAKMIRYFYNAKAGLCQPFYGGGRASNPNFKSADDCNRTCGA 59

RESULT 3
SI0063
Isoaprotinin G2 - bovine hybrid
C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: SI0063
Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
Bio1.Stiekman, J.; Menzel, H.R.; Schroeder, W.; Tschesche, H.
ArTitle: Characterization and sequence determination of six aprotinin homologues from boar
A:Reference number: S00371; MUID:88221840; PMID:2453200
A:Accession: SI0063
A:Molecule type: Protein
A:Residues: 1-58 <SI>
A:Cross-references: UNIPROT:Q7MJ12
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homology <BPI>
C:Keywords: serine proteinase inhibitor
P:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
P:15/inhibitory site: Lys (trypsin) #status predicted
```

Query Match	57.1%	Score 188	DB 2	Length 58
Local Similarity	56.1%	Pred. No. 4.7e-16		
Matches	32	Conservative 8	Mismatches 17	Indels 0
			Gaps	0
QY	2	PVRLCLLPATGSPCARIRIRYFVASVGGCNRFYGGCGGNANNTAFSEDECHSSCGGS	58	
		.....		
DB	2	PDFCLLEPPYGPCCARMIRYFNKAGLCGCFYVGGCCAKRNNTKSSMEDCRTGTGGA	58	
		.....		

RESULT 4  
TIBOR  
serum basic proteinase inhibitor - bovine  
C|Species: Bos primigenius taurus (cattle)  
C|Date: 31-Oct-1980 #sequence\_revision 31-Oct-1980 #text\_change 09-Jul-2004  
C|Accession: A01206  
R|Wachter, E.; Degener, K.; Hochstrasser, K.; Lempart, K.; Geiger, R.  
FEBS Lett. 119, 58-62, 1980  
A|Title: A new Kunitz-type inhibitor from bovine serum amino acid sequence determination  
A|Reference number: A01206; MUID:81044408; PMID:7428928  
A|Accession: A01206  
A|Molecule type: protein  
A|Residues: 1-60 <MAC>  
A|Cross-references: UNIPROT:P00975  
C|Comment: This inhibitor has activity very similar to that of the basic protease inhibitor  
C|Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog



A:Molecule type: DNA  
 A:Residues: 1-111 <PRT>  
 A:Cross-references: UNIPROT:Q7M4L3  
 F:59-109/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 51.1%; Score 168; DB 2; Length 111;  
 Best Local Similarity 55.8%; Pred. No. 2.4e-13;  
 Matches 29; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 5 CULPPTGPKARIIRWYFVASVGQCNRFYGGCGGNANFPASBQECMSSCQ 56  
 DB 59 CSQEAMTGPCRAVMPRWYFDLSKSKCVRFYGGCGGNRNNFESBDCMAVCK 110

RESULT 8  
 A49974  
 beta-amyloid precursor protein 2 homolog APLP2 - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C:Accession: A49974  
 R:Jlunt, H.H.; Tinkaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.  
 J. Biol. Chem. 269, 2637-2644, 1994  
 A>Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid  
 A:Reference number: A49974; WUID:94132029; PMID:830594  
 A:Accession: A49974  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-751 <SLU>  
 A:Cross-references: UNIPROT:Q60709; GB:U1571; NID:9558467; PIDN:AA50603.1; PID:9558468  
 A:Note: Sequence extracted from NCBI backbone (NCBI:P:144636)  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 F:110-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 51.1%; Score 168; DB 2; Length 751;  
 Best Local Similarity 55.8%; Pred. No. 1.4e-12;  
 Matches 29; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 5 CULPPTGPKARIIRWYFVASVGQCNRFYGGCGGNANFPASBQECMSSCQ 56  
 DB 310 CSQEAMTGPCRAVMPRWYFDLSKSKCVRFYGGCGGNRNNFESBDCMAVCK 361

RESULT 9  
 A49321  
 amyloid beta (A4) homolog 2 precursor - human  
 N:Alternate names: CDE1-binding protein  
 C:Species: Homo sapiens (man)  
 C>Date: 24-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C:Accession: A49321; S34644; S40519  
 R:Spreecher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster,  
 Biochemistry 32, 4461-4466, 1993  
 A>Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: ev  
 A:Reference number: A49321; WUID:93250009; PMID:8485127  
 A:Accession: A49321  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-763 <SPR>  
 A:Cross-references: UNIPROT:Q06481; GB:S60099; NID:9300168; PIDN:AA60589.1; PID:9300169  
 A:Experimental source: placenta  
 A:Note: Sequence extracted from NCBI backbone (NCBI:N:131198, NCBI:P:131199)  
 A:Note: expression was shown in placenta, brain, heart, lung, liver, and kidney  
 R:yon der Kammer, H.; Kladinsky, J.; Hanes, J.; Scheitel, K.H.  
 submitted to the EMBL Data Library, April 1993  
 A:Description: The human homologue of the murine CDE1 binding protein is an amyloid prec  
 A:Reference number: S34644  
 A:Accession: S34644  
 A:Molecule type: mRNA  
 A:Residues: 1-763 <YON>  
 A:Cross-references: EMBL:222572; NID:9394763; PIDN:CAA80295.1; PID:9394764  
 R:Wassco, W.; Gurtubagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.;  
 Nature Genet. 5, 95-99, 1993  
 A>Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's  
 A:Reference number: S40519; WUID:94053131; PMID:8220435

A:Accession: S40519  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-763 <WAS>  
 A:Cross-references: GB:L27631; NID:9450391; PIDN:AA41701.1; PID:9450392  
 C:Genetic: S40519  
 A:Gene: GDB:APLP2; APLP2  
 A:Cross-references: GDB:139159; OMIM:104776  
 A:Map position: 11q23-11q25  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 F:110-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 51.1%; Score 168; DB 2; Length 763;  
 Best Local Similarity 55.8%; Pred. No. 1.4e-12;  
 Matches 29; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 5 CULPPTGPKARIIRWYFVASVGQCNRFYGGCGGNANFPASBQECMSSCQ 56  
 DB 310 CSQEAMTGPCRAVMPRWYFDLSKSKCVRFYGGCGGNRNNFESBDCMAVCK 361

RESULT 10  
 S42880  
 amyloid precursor-like protein - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 C:Accession: S42880; S47528  
 R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.  
 submitted to the EMBL Data Library, March 1994  
 A:Description: Complete nucleotide ad deduced amino acid sequence of rat amyloid precurs  
 A:Reference number: S42880  
 A:Accession: S42880  
 A:Molecule type: mRNA  
 A:Residues: 1-765 <SAN>  
 A:Cross-references: UNIPROT:P15943; EMBL:X77934  
 R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.  
 Biochim. Biophys. Acta 1219, 167-170, 1994  
 A>Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein prec  
 A:Reference number: S47528; WUID:94368849; PMID:8086458  
 A:Accession: S47528  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-765 <SAB>  
 A:Cross-references: EMBL:X77934  
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase  
 F:112-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 51.1%; Score 168; DB 2; Length 765;  
 Best Local Similarity 55.8%; Pred. No. 1.4e-12;  
 Matches 29; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 5 CULPPTGPKARIIRWYFVASVGQCNRFYGGCGGNANFPASBQECMSSCQ 56  
 DB 312 CSQEAMTGPCRAVMPRWYFDLSKSKCVRFYGGCGGNRNNFESBDCMAVCK 363

RESULT 11  
 TIVIT1  
 venom basic proteinase inhibitor I - western sand viper  
 N:Alternate names: venom trypsin inhibitor I  
 C:Species: Vipera ammodytes ammodytes (western sand viper)  
 C>Date: 19-Feb-1984 #sequence\_revision 19-Feb-1984 #text\_change 09-Jul-2004  
 C:Accession: A01222  
 R:Rittonja, A.; Meloun, B.; Gubensek, F.  
 Biochim. Biophys. Acta 740, 429-435, 1983  
 A>Title: The primary structure of Vipera ammodytes venom trypsin inhibitor I.  
 A:Reference number: A01222; WUID:84053385; PMID:6639951  
 A:Accession: A01222  
 A:Molecule type: Protein  
 A:Residues: 1-61 <RTV>  
 A:Cross-references: UNIPROT:P00991

C:Comment: This protein inhibits trypsin and kallikrein.  
C:Superfamily: basic proteinase inhibitor; animal knittz-type proteinase inhibitor  
C:Keywords: pyroglutamic acid; serine proteinase inhibitor; venom  
F:7-57/Domains: animal knittz-type proteinase inhibitor homology <BPT>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:7-57,16-40,32-53/Disulfide bonds: #status predicted  
F:11/inhibitory site: Lys (trypsin) #status predicted

Query Match	49.8%	Score 164	DB 1	Length 61
Best Local Similarity	48.3%	Pred. No. 4.2e-13		
Matches 28	Conservative 10	Mismatches 20	Indels 0	Gaps 0

QY 1 YPVRCLLPPATGPCCKARIIRWYFVASVGQCNREYVYGGCRGNANNFASDEQCMSSCGGS 58  
: | | | | | : : : : | | | | | : | | : |  
Db 3 HPKFCYLPADPGRCKAHIFRFYDASAKCNKFIYGGCRGNANNFKTWDECRQTGAS 60

**RESULT 12**

basic proteinase inhibitor - great pond snail  
N/Alternate names: trypsin inhibitor  
C/Species: *Lymanaea stagnalis* (great pond snail)  
C/Date: 04-Mar-2000 #sequence\_revision 04-Mar-2000 #text\_change 09-Jul-2004  
C/Accession: A59204  
R/Magle, G.  
submitted to the Protein Sequence Database, March 2000  
A/Description: *Lymanaea* trypsin inhibitor.  
A/Reference number: A59204

A:Molecule type: protein  
A:Residues: 1-57 <NG>  
A:Cross-references: UNIPROT:Q7M411  
A:Experimental source: albunen gland  
C:Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor  
C:Keywords: glycoprotein; serine proteinase inhibitor  
F:5-55/Domain: animal kunitz-type proteinase inhibitor homology <BPI>  
F:5-55\_14-38\_30-51/Disulfide bonds: #status predicted  
F:15/Inhibitory site: lys (tryptin) #status predicted  
F:24/Binding site: carbohydrate (asn) (covalent) #status experimental

Qy 5 CLEPATGPKARIRWYFVASVGQCNRVYGGCGGNANFASBQECMSSC 55  
| | | | | : : : : | : | | | | | : : : |  
Db 5 CSLPSETGPKCNFLRHYHSSSTNACDSVYGGCGGNANFQDIDDCAKC 55

### RESULT 13

A44180  
talicotoxin serine proteinase inhibitor component - Australian taipan  
C/Species: Oxyuranus scutellatus scutellatus (Australian taipan)  
C/Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: A44180  
R/Possani, L.D.; Martin, B.M.; Yatani, A.; Mochoa-Morales, J.; Zamudio, F.Z.; Gurrola, G.  
Toxicom 30, 1343-1364, 1992  
A/Title: Isolation and physiological characterization of talicotoxin, a complex toxin with  
A/Reference number: A44180; MUID:93134601; PMID:1465334  
A/Accession: A44180  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-62 <POS>  
A/Cross-references: UNIPROT:Q7LZE4  
A/Experimental source: subsp. scutellatus, venom  
A/Note: sequence extracted from NCBI backbone (NCBI:122482)  
C/Superfamily: basic proteinase inhibitor; animal kunitz-type proteinase inhibitor homol  
C/Keywords: serine proteinase inhibitor  
C/57/Domin: animal kunitz-type proteinase inhibitor homology <BPI>

Query Match	49.5%	Score 163	DB 2	Length 62
Best Local	50.0%	Pred. No. 5.6e-13		
Matches 28	Conservative	7	Mismatches 21	Indels 0
			Gaps	0

```

Qy      2  PVRCLLPATGPECKARIIRMYFVASVGQCNRIVYGGCRGNANNPASSEQECSSCOG  57
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      4  PKFCHLPPKPGPCRAIPRFYYNPHSKQCEKFIYGGCHGNANKFKTPDECNVYTCLG  59

```

RESULT 14  
TITTOR

```
basic proteinase inhibitor - loggerhead
CISpecies: Caretta caretta (loggerhead)
CDate: 31-May-1979 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
```

```

Query Match 163;   Score 163;   DB 1;   Length 110;
Best Local Similarity 48.1%;   Pred. No. 9.5e-13;
Matches 25;   Conservative 11;   Mismatches 16;   Gaps 0

```

Qy 5 CILPPATGPEKARIIRWYFVASVQCNRFYGGCGKGNANFPASEDECMSSCQ 56  
 Db 8 CILPPGEGCKGRIPRYFYNPASBMCEFTYGGCKGNKNFKTKAEVRACR 59

## RESULT 15

hypochemical protein R12A1.3 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C:Accession: J132060  
 R:Pauley, A., Andrews, S.  
 submitted to the EMBL Data Library, July 1997  
 A:Description: The sequence of C. elegans cosmid R12A1.  
 A:Reference number: J21118  
 A:Accession: J132060  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-249 <PAU>  
 A:Cross-references: UNIPROT:O16701; EMBL:AF016680; PIDN:ABE6164.1; GSPDB:GN00023; CESP:P  
 C:Experimental source: strain Bristol N2; clone R12A1  
 C:Genetics:  
 A:Gene: CESP:R12A1.3  
 A:Map position: 5  
 A:introns: 75/1, 139/1

Query Match	48.9%	Score 161	DB 2	Length 249
Best Local Similarity	55.6%	Pred. No. 3.5e-12		
Matches 30; Conservative	8	Mismatches 12	Indels 4	Gaps 1

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Oy      5  CILPPATGPKARIIRWYFVAVSGQCNRFYGGCRGNANNFASEQECCSSCQGS  58
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      143 CSLPLAVSCTAPAVRFYDYDASSGRCNQEMYSGCCGNANNFOS----LSSCQGT  192

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Search completed: August 25, 2005, 04:55:46  
Job time : 17 secs



**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2005, 04:48:53 ; Search time 25 Seconds  
(without alignments)  
173.186 Million cell updates/sec

Title: US-10-721-961-4

Perfect score: 329  
Sequence: 1 YPVRCILPPATGPKARIIR.....RGNNANFASBOECMSSCGS 58

Scoring table: BLASTSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	264	80.2	58	3	US-09-369-494-1
2	264	80.2	58	4	US-09-369-670-1
3	264	80.2	189	3	US-09-369-494-15
4	264	80.2	189	4	US-09-369-670-15
5	220.5	67.0	51	3	US-09-369-494-9
6	220.5	67.0	51	4	US-09-369-670-9
7	208	63.2	109	1	US-08-084-718-75
8	208	63.2	109	1	US-08-443-976-75
9	208	63.2	109	1	US-08-443-977-75
10	203	61.7	111	1	US-08-084-718-59
11	203	61.7	111	1	US-08-443-976-59
12	203	61.7	111	1	US-08-443-977-59
13	202	61.4	109	1	US-08-084-718-71
14	202	61.4	109	1	US-08-443-976-71
15	202	61.4	109	1	US-08-443-977-71
16	198	60.2	141	1	US-08-084-718-69
17	198	60.2	141	1	US-08-443-976-69
18	198	60.2	141	1	US-08-443-977-69
19	194	59.0	58	1	US-08-084-718-41
20	194	59.0	58	1	US-08-443-976-41
21	194	59.0	58	1	US-08-443-977-41
22	194	59.0	111	1	US-08-084-718-61
23	194	59.0	111	1	US-08-443-976-61
24	194	59.0	111	1	US-08-443-977-61
25	194	59.0	141	1	US-08-084-718-81
26	194	59.0	141	1	US-08-084-718-81
27	194	59.0	141	1	US-08-443-976-77

28	194	59.0	141	1	US-08-443-976-81	Sequence 81, Appl
29	194	59.0	141	1	US-08-443-977-77	Sequence 77, Appl
30	194	59.0	141	1	US-08-443-977-81	Sequence 81, Appl
31	193	58.7	56	1	US-07-598-737C-33	Sequence 33, Appl
32	193	58.7	56	1	US-08-084-718-34	Sequence 34, Appl
33	193	58.7	56	1	US-08-443-976-34	Sequence 34, Appl
34	193	58.7	56	1	US-08-443-977-34	Sequence 34, Appl
35	193	58.7	57	4	US-08-896-322-5	Sequence 5, Appl1
36	193	58.7	141	1	US-08-084-718-65	Sequence 65, Appl
37	193	58.7	141	1	US-08-084-718-73	Sequence 73, Appl
38	193	58.7	141	1	US-08-443-976-65	Sequence 65, Appl
39	193	58.7	141	1	US-08-443-976-73	Sequence 73, Appl
40	193	58.7	141	1	US-08-443-977-65	Sequence 65, Appl
41	193	58.7	141	1	US-08-443-977-73	Sequence 73, Appl
42	192	58.4	58	1	US-07-664-989B-44	Sequence 44, Appl
43	192	58.4	58	1	US-07-598-737C-1	Sequence 1, Appl1
44	192	58.4	58	1	US-08-084-718-1	Sequence 1, Appl1
45	192	58.4	58	1	US-08-084-718-39	Sequence 39, Appl

## ALIGNMENTS

RESULT 1  
US-09-369-494-1  
Sequence 1, Application US/09369494  
Patent No. 6180607  
GENERAL INFORMATION:  
APPLICANT: Davies, Christopher  
APPLICANT: Chen, Dandong  
TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity  
FILE REFERENCE: MSB-7260  
CURRENT FILING DATE: 1999-08-05  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 58  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: fragment from  
US-09-369-494-1

Query Match 80.2%; Score 264; DB 3; Length 58;  
Best Local Similarity 82.8%; Pred. No. 1.7e-25;  
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 YPVRCILPPATGPKARIIRVYVAVSGCNRVYGGCGNNANFASBOECMSSCGS 58  
DB 1 YPVRCILPPATGPKARIIRVYVAVSGCNRVYGGCGNNANFASBOECMSSCGS 58

RESULT 2  
US-09-569-670-1  
Sequence 1, Application US/09569670  
Patent No. 6689582  
GENERAL INFORMATION:  
APPLICANT: Davies, Christopher  
APPLICANT: Chen, Dandong  
TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity  
FILE REFERENCE: MSB-7260  
CURRENT FILING DATE: 2000-05-12  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 58  
TYPE: PRT  
ORGANISM: Artificial Sequence

binding site

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FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-569-670-1
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Query Match      80.2%; Score 264; DB 4; Length 58;
Best Local Similarity 82.8%; Pred. No.1.7e-25;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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Qy      1 YPVRCLLPATGPKARIIRWYFVASVGQCNRFVYGGCGGNANNNFASBQECMSSCGS 58
Db      1 YPVRCLLPSAHGSCADWAARWYFVASVGQCNRFWYGGCHGNANNNFASBQECMSSCGS 58
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RESULT 3
US-09-369-494-15
; Sequence 15, Application US/09369494
; Patent No. 6180607
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznik, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/369,494
; CURRENT FILING DATE: 1999-08-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-369-494-15
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Query Match      80.2%; Score 264; DB 3; Length 189;
Best Local Similarity 82.8%; Pred. No.5.9e-25;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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Db      10 YPVRCLLPSAHGSCADWAARWYFVASVGQCNRFWYGGCHGNANNNFASBQECMSSCGS 67
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RESULT 4
US-09-569-670-15
; Sequence 15, Application US/09569670
; Patent No. 6689582
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznik, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/569,670
; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-569-670-15
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Query Match      80.2%; Score 264; DB 4; Length 189;
Best Local Similarity 82.8%; Pred. No.5.9e-25;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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Qy      1 YPVRCLLPATGPKARIIRWYFVASVGQCNRFVYGGCGGNANNNFASBQECMSSCGS 58
Db      10 YPVRCLLPSAHGSCADWAARWYFVASVGQCNRFWYGGCHGNANNNFASBQECMSSCGS 67
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RESULT 5
US-09-369-494-9
; Sequence 9, Application US/09369494
; Patent No. 6180607
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznik, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/369,494
; CURRENT FILING DATE: 1999-08-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-369-494-9
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Query Match      67.0%; Score 220.5; DB 3; Length 51;
Best Local Similarity 80.8%; Pred. No.3.4e-20;
Matches 42; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
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Qy      5 CLLPATGPKARIIRWYFVASVGQCNRFVYGGCGGNANNNFASBQECMSSCG 56
Db      1 CLLPSAHGSCADWAARWYFVASVGQCNRFWYGGC-GNANNNFASBQECMSSCG 51
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RESULT 6
US-09-569-670-9
; Sequence 9, Application US/09569670
; Patent No. 6689582
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznik, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/569,670
; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-569-670-9
```

```
Query Match      67.0%; Score 220.5; DB 4; Length 51;
Best Local Similarity 80.8%; Pred. No.3.4e-20;
Matches 42; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
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Qy      5 CLLPATGPKARIIRWYFVASVGQCNRFVYGGCGGNANNNFASBQECMSSCG 56
Db      1 CLLPSAHGSCADWAARWYFVASVGQCNRFWYGGC-GNANNNFASBQECMSSCG 51
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```
RESULT 7
US-08-084-718-75
; Sequence 75, Application US/08084718
; Patent No. 5591603
```

GENERAL INFORMATION:  
APPLICANT: Bjorn, Soeren E.  
APPLICANT: No. 5591603xis, Kjeld  
APPLICANT: Diness, Viggo  
APPLICANT: No. 5591603xkov-Lauritsen, Leif  
APPLICANT: Christensen, Niels D.  
APPLICANT: Bregengaard, Claus  
APPLICANT: No. 5591603xis, Fanny  
APPLICANT: Petersen, Lars C.  
TITLE OF INVENTION: Process for the Preparation of Aprotinin  
TITLE OF INVENTION: and Aprotinin Analogs  
NUMBER OF SEQUENCES: 83  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5591603 No. 5591603disk of No. 5591603th America, Inc.  
STREET: 405 Lexington Avenue, 62nd Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/084,718  
FILING DATE: 19930623  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 4501/87  
FILING DATE: 28-AUG-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 2254/88  
FILING DATE: 26-APR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK88/00138  
FILING DATE: 28-AUG-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK89/00096  
FILING DATE: 25-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/466,408  
FILING DATE: 21-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 2361/90  
FILING DATE: 01-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/598,337  
FILING DATE: 19-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 1118/91  
FILING DATE: 12-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK91/00299  
FILING DATE: 01-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,687  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/024,925  
FILING DATE: 26-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Agri's, Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3143,224-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-867-0298  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-084-718-75  
Query Match 63.2%; Score 208; DB 1; Length 109;  
Best Local Similarity 63.0%; Pred. No.2.6e-18;  
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;  
Qy 5 CLLPATGPKAKIRIRYFVAVGQCNRPYVGCGRGNANNFASBOECMSSCGGS 58  
Db 56 CLPSTGPKAKIRIRYFNAKAGLCQTFYVGCGRGNANNFASBOECMTCGA 109  
RESULT 8  
US-08-443-976-75  
Sequence 75, Application US/08443976  
Patent No. 5618915  
GENERAL INFORMATION:  
APPLICANT: Bjorn, Soeren E.  
APPLICANT: No. 5618915xis, Kjeld  
APPLICANT: Diness, Viggo  
APPLICANT: No. 5618915xkov-Lauritsen, Leif  
APPLICANT: Christensen, Niels D.  
APPLICANT: Bregengaard, Claus  
APPLICANT: No. 5618915xis, Fanny  
APPLICANT: Petersen, Lars C.  
TITLE OF INVENTION: Process for the Preparation of Aprotinin  
TITLE OF INVENTION: and Aprotinin Analogs  
NUMBER OF SEQUENCES: 83  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5618915 No. 5618915disk of No. 5618915th America, Inc.  
STREET: 405 Lexington Avenue, 62nd Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/443,976  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/084,718  
FILING DATE: 23-JUN-1993  
APPLICATION NUMBER: DK 4501/87  
FILING DATE: 28-AUG-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 2254/88  
FILING DATE: 26-APR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK88/00138  
FILING DATE: 28-AUG-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK89/00096  
FILING DATE: 25-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/466,408  
FILING DATE: 21-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 2361/90  
FILING DATE: 01-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/598,337  
FILING DATE: 19-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 1118/91  
FILING DATE: 12-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK91/00299  
FILING DATE: 01-OCT-1991

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,687  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/024,925  
FILING DATE: 26-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Agtis, Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3143.224-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-867-0298  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-443-976-75

Query Match 63.2%; Score 208; DB 1; Length 109;  
Best local Similarity 63.0%; Pred. No. 2.6e-18;  
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 5 CLPPTGPKKARIIRYFVNASVGCNRPVYGGCRGNANFASBQECMSSCGS 58  
Db 56 CLEPSTGPKARIIRYFYNAKAGLCQTFVYGGCRGNNGNPFSAEDCMETCGA 109

RESULT 9  
US-08-443-977-75  
Sequence 75, Application US/08443977  
Patent No. 5621074  
GENERAL INFORMATION:  
APPLICANT: Bjorn, Soeren E.  
APPLICANT: No. 5621074r1s, Kjeld  
APPLICANT: Dinesb, Viggo  
APPLICANT: No. 5621074rskov-Lauritsen, Lelf  
APPLICANT: Christensen, Niels D.  
APPLICANT: Bregengaard, Claus  
APPLICANT: No. 5621074r1s, Fanny  
APPLICANT: Petersen, Lars C.  
TITLE OF INVENTION: Process for the Preparation of Aprotinin  
NUMBER OF SEQUENCES: 83  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 56210740 No. 5621074disk of No. 5621074th America, Inc.  
STREET: 405 Lexington Avenue, 62nd Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/443,977  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/084,718  
FILING DATE: 23-JUN-1993  
APPLICATION NUMBER: DK 4561/87  
FILING DATE: 28-AUG-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 2254/88  
FILING DATE: 26-APR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK88/00138  
FILING DATE: 28-AUG-1988

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK89/00096  
FILING DATE: 25-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/466,408  
FILING DATE: 21-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 2361/90  
FILING DATE: 01-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/598,337  
FILING DATE: 19-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 1118/91  
FILING DATE: 12-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK91/00299  
FILING DATE: 01-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,687  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/024,925  
FILING DATE: 26-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Agtis, Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3143.224-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-867-0298  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-443-977-75

Query Match 63.2%; Score 208; DB 1; Length 109;  
Best local Similarity 63.0%; Pred. No. 2.6e-18;  
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 5 CLPPTGPKKARIIRYFVNASVGCNRPVYGGCRGNANFASBQECMSSCGS 58  
Db 56 CLEPSTGPKARIIRYFYNAKAGLCQTFVYGGCRGNNGNPFSAEDCMETCGA 109

RESULT 10  
US-08-084-718-59  
Sequence 59, Application US/08084718  
Patent No. 5591603  
GENERAL INFORMATION:  
APPLICANT: Bjorn, Soeren E.  
APPLICANT: No. 5591603r1s, Kjeld  
APPLICANT: Dinesb, Viggo  
APPLICANT: No. 5591603rskov-Lauritsen, Lelf  
APPLICANT: Christensen, Niels D.  
APPLICANT: Bregengaard, Claus  
APPLICANT: No. 5591603r1s, Fanny  
APPLICANT: Petersen, Lars C.  
TITLE OF INVENTION: Process for the Preparation of Aprotinin  
NUMBER OF SEQUENCES: 83  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 55916030 No. 5591603disk of No. 5591603th America, Inc.  
STREET: 405 Lexington Avenue, 62nd Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/084,718
FILING DATE: 19930623
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 4501/87
FILING DATE: 28-AUG-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2254/88
FILING DATE: 26-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00138
FILING DATE: 28-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK89/00096
FILING DATE: 25-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/466,408
FILING DATE: 21-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2361/90
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/598,337
FILING DATE: 19-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1118/91
FILING DATE: 12-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00299
FILING DATE: 01-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,687
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,925
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Agtis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3143.224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-084-718-59

Query Match 61.7%; Score 203; DB 1; Length 111;
Best Local Similarity 59.6%; Pred. No. 1,1e-17;
Matches 34; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

```

```

APPLICANT: Christensen, Niels D.
APPLICANT: Bregengaard, Claus
APPLICANT: No. 56189151s, Fanny
APPLICANT: Petersen, Lars C.
TITLE OF INVENTION: Process for the Preparation of Aprotinin
TITLE OF INVENTION: and Aprotinin Analogs
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESSES:
ADDRESS: No. 56189150 No. 5618915disk of No. 5618915th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,976
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,718
FILING DATE: 23-JUN-1993
APPLICATION NUMBER: DK 4501/87
FILING DATE: 28-AUG-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2254/88
FILING DATE: 26-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK88/00138
FILING DATE: 28-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK89/00096
FILING DATE: 25-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/466,408
FILING DATE: 21-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 2361/90
FILING DATE: 01-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/598,337
FILING DATE: 19-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 1118/91
FILING DATE: 12-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00299
FILING DATE: 01-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,687
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,925
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Agtis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3143.224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-443-976-59

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Query Match 61.7%; Score 203; DB 1; Length 111;  
Best Local Similarity 59.6%; Pred. No. 1,1e-17;  
Matches 34; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 2 PVRCLEPPTGPKARIRIRYFVASVQGNRFYVGGCRGNANFPASBOECMSSCOGS 58  
DB 55 PDCLEBPSTGPKARIRIRYFVDATAGLCETFYVGGCRANRNNFKSABDCEMTCGGA 111

RESULT 12  
US-08-443-977-59  
Sequence 59, Application US/08443977  
Patent No. 5621074  
GENERAL INFORMATION:  
APPLICANT: Bjorn, Soeren E.  
APPLICANT: No. 5621074xis, Kjeld  
APPLICANT: Dines, Viggo  
APPLICANT: No. 5621074rakov-Lauritsen, Lelf  
APPLICANT: Christensen, Niels D.  
APPLICANT: Bregengaard, Claus  
APPLICANT: No. 5621074xis, Fanny  
APPLICANT: Petersen, Lars C.  
TITLE OF INVENTION: Process for the Preparation of Aprotinin  
TITLE OF INVENTION: and Aprotinin Analogs  
NUMBER OF SEQUENCES: 83  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 56210740 No. 5621074disk of No. 5621074ch America, Inc.  
STREET: 405 Lexington Avenue, 62nd Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/443,977  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
APPLICATION NUMBER: US 08/084,718  
PRIOR APPLICATION DATA:  
FILING DATE: 23-JUN-1993  
APPLICATION NUMBER: DK 4501/87  
FILING DATE: 28-AUG-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 2254/88  
FILING DATE: 26-APR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK88/00138  
FILING DATE: 28-AUG-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK89/00096  
FILING DATE: 25-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/466,408  
FILING DATE: 21-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 2361/90  
FILING DATE: 01-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 1118/91  
FILING DATE: 12-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK91/00299  
FILING DATE: 01-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,687  
FILING DATE: 29-JAN-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/024,925  
FILING DATE: 26-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Agtis, Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3143.224-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-867-0298  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-443-977-59

Query Match 61.7%; Score 203; DB 1; Length 111;  
Best Local Similarity 59.6%; Pred. No. 1,1e-17;  
Matches 34; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 2 PVRCLEPPTGPKARIRIRYFVASVQGNRFYVGGCRGNANFPASBOECMSSCOGS 58  
DB 55 PDCLEBPSTGPKARIRIRYFVDATAGLCETFYVGGCRANRNNFKSABDCEMTCGGA 111

RESULT 13  
US-08-084-718-71  
Sequence 71, Application US/08084718  
Patent No. 5591603  
GENERAL INFORMATION:  
APPLICANT: Bjorn, Soeren E.  
APPLICANT: No. 5591603xis, Kjeld  
APPLICANT: Dines, Viggo  
APPLICANT: No. 5591603rakov-Lauritsen, Lelf  
APPLICANT: Christensen, Niels D.  
APPLICANT: Bregengaard, Claus  
APPLICANT: No. 5591603xis, Fanny  
APPLICANT: Petersen, Lars C.  
TITLE OF INVENTION: Process for the Preparation of Aprotinin  
TITLE OF INVENTION: and Aprotinin Analogs  
NUMBER OF SEQUENCES: 83  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 55916030 No. 5591603disk of No. 5591603ch America, Inc.  
STREET: 405 Lexington Avenue, 62nd Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/084,718  
FILING DATE: 19930623  
CLASSIFICATION: 514  
APPLICATION NUMBER: PCT/DK88/00138  
FILING DATE: 28-AUG-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 2254/88  
FILING DATE: 26-APR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK88/00138  
FILING DATE: 28-AUG-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK89/00096  
FILING DATE: 25-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/466,408



FILING DATE: 21-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 2361/90  
FILING DATE: 01-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/598,337  
FILING DATE: 19-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 1118/91  
FILING DATE: 12-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK91/00239  
FILING DATE: 01-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,687  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/024,925  
FILING DATE: 26-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Agriis, Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3143, 224-US  
TELEPHONE: 212-867-0123  
TELEFAX: 212-867-0298  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-084-718-71

Query Match 61.4%; Score 202; DB 1; Length 109;  
Best Local Similarity 61.1%; Pred. No. 1,4e-17;  
Matches 33; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 5 CLLPATGPKARIIRYFYASVQGNRFYGGCGRGNANNPASBQCMSSCGGS 58  
Db 56 CLPPTGPKARIIRYFYDATAGLCETFYGGCGRANRNPFSAEDCMETCGGA 109

RESULT 14  
US-08-443-976-71  
Sequence 71, Application US/08443976  
Patent No. 5618915  
GENERAL INFORMATION:  
APPLICANT: Bjorn, Soeren E.  
APPLICANT: No. 5618915r1s, Kjeld  
APPLICANT: Diness, Viggo  
APPLICANT: No. 5618915rskov-Lauritsen, Leif  
APPLICANT: Christensen, Niels D.  
APPLICANT: Brengsaard, Claus  
APPLICANT: No. 5618915r1s, Fanny  
APPLICANT: Petersen, Lars C.  
TITLE OF INVENTION: Process for the Preparation of Aprotinin  
TITLE OF INVENTION: and Aprotinin Analogs  
NUMBER OF SEQUENCES: 83  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: No. 5618915dsk of No. 5618915th America, Inc.  
STREET: 405 Lexington Avenue, 62nd Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/443,976

FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/084,718  
FILING DATE: 23-JUN-1993  
APPLICATION NUMBER: DK 4501/87  
FILING DATE: 28-AUG-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 2254/88  
FILING DATE: 26-APR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK88/00138  
FILING DATE: 28-AUG-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK89/00096  
FILING DATE: 25-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/466,408  
FILING DATE: 21-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 2361/90  
FILING DATE: 01-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/598,337  
FILING DATE: 19-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 1118/91  
FILING DATE: 12-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK91/00299  
FILING DATE: 01-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,687  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/024,925  
FILING DATE: 26-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Agriis, Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3143, 224-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-867-0298  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-443-976-71

Query Match 61.4%; Score 202; DB 1; Length 109;  
Best Local Similarity 61.1%; Pred. No. 1,4e-17;  
Matches 33; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 5 CLLPATGPKARIIRYFYASVQGNRFYGGCGRGNANNPASBQCMSSCGGS 58  
Db 56 CLPPTGPKARIIRYFYDATAGLCETFYGGCGRANRNPFSAEDCMETCGGA 109

RESULT 15  
US-08-443-977-71  
Sequence 71, Application US/08443977  
Patent No. 5621074  
GENERAL INFORMATION:  
APPLICANT: Bjorn, Soeren E.  
APPLICANT: No. 5621074r1s, Kjeld  
APPLICANT: Diness, Viggo  
APPLICANT: No. 5621074rskov-Lauritsen, Leif  
APPLICANT: Christensen, Niels D.  
APPLICANT: Brengsaard, Claus  
APPLICANT: No. 5621074r1s, Fanny

APPLICANT: Petersen, Lars C.  
TITLE OF INVENTION: Process for the Preparation of Aprotinin  
TITLE OF INVENTION: and Aprotinin Analogs  
NUMBER OF SEQUENCES: 83  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: No. 56210740 No. 5621074disk of No. 5621074th America, Inc.  
STREET: 405 Lexington Avenue, 62nd Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/443,977  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/084,718  
FILING DATE: 23-JUN-1993  
APPLICATION NUMBER: DK 4501/87  
FILING DATE: 28-AUG-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 2254/88  
FILING DATE: 26-APR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK88/00138  
FILING DATE: 28-AUG-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK89/00096  
FILING DATE: 25-APR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/466,408  
FILING DATE: 21-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 2361/90  
FILING DATE: 01-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/598,337  
FILING DATE: 19-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 1118/91  
FILING DATE: 12-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK91/00299  
FILING DATE: 01-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,687  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/024,925  
FILING DATE: 26-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Agtis, Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3143.224-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-867-0298  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-443-977-71

Query Match 61.4%; Score 202; DB 1; Length 109;  
Best Local Similarity 61.1%; Pred. No. 1,4e-17;  
Matches 33; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 5 CILPATGCKARIRRMVFSVSGQNRFYGGCGRNNANFASBQECMSCCGS 58  
DB 56 CLEPSTGCKARIRRYFDATAGLCETFYGGCRANRRNFRKSABDCMETCGGA 109

Search completed: August 25, 2005, 04:56:24  
Job time : 33 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2005, 04:45:06 ; Search time 176 Seconds  
(without alignments)  
168.753 Million cell updates/sec

Title: US-10-721-961-4  
Perfect score: 329  
Sequence: 1 YPVRCLLPATGPCKARIR.....RGNNANFASBQECMSSCGGS 58

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1613378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1613378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	264	80.2	531	2	Q659F2
2	264	80.2	531	2	Q6ZNM1
3	264	80.2	531	2	Q7Z6B1
4	264	80.2	531	2	Q95A28
5	246	74.8	1280	2	Q9EPX2
6	190	58.4	100	1	BPT1_BOVIN
7	190	57.8	59	2	Q7M311
8	188	57.1	58	2	Q7M312
9	186	56.5	984	2	Q9GON1
10	186	56.5	984	2	Q9GON2
11	185	56.2	327	2	Q6IND9
12	184	55.9	60	1	IBPS_BOVIN
13	184	55.9	100	1	BPT2_BOVIN
14	177	53.8	82	2	Q7Z2T3
15	174	52.9	122	1	UPT1_PIG
16	172	52.3	80	2	Q8T357
17	168	51.1	111	2	Q7M413
18	168	51.1	523	2	Q14594
19	168	51.1	738	2	Q90W28
20	168	51.1	738	2	Q6NUZ1
21	168	51.1	751	2	Q60709
22	168	51.1	753	1	APP2_HUMAN
23	168	51.1	753	2	Q71U10
24	168	51.1	763	2	Q61482
25	168	51.1	765	1	APP2_RAT
26	166	50.5	283	2	Q6ZNT4
27	166	50.5	576	2	Q8TEU8
28	166	50.2	576	2	Q6UX29
29	165	50.2	82	2	Q8WV44
30	165	50.2	83	2	Q90WA0
31	165	50.2	252	1	SPT2_HUMAN

32	165	50.2	252	2	Q6LEU8	Q6LEU8 homo sapien
33	164	49.8	61	1	IVB1_VIPAA	P00591 vipera ammo
34	164	49.8	90	2	Q6XPY8	Q6XPY8 vipera ammo
35	163	49.5	57	2	Q7M411	Q7M411 lymnaea sta
36	163	49.5	62	1	IVBT_OXYSC	Q7124 oxyuranus s
37	163	49.5	110	1	IBP_CARCR	P00993 caretta car
38	163	49.5	193	2	Q6P796	Q6P796 rattus norv
39	163	49.5	571	2	Q7TQN3	Q7TQN3 mus muscula
40	162	49.2	58	1	AXPI_ANTAF	P81547 anthopleura
41	162	49.2	58	1	Q9TW99	Q9TW99 anemonia su
42	162	49.2	83	2	Q90W98	Q90W98 pseudonaja
43	161	48.9	133	2	Q8HZ45	Q8HZ45 papio papio
44	161	48.9	253	2	Q16701	Q16701 caenorhabdi
45	161	48.9	751	2	Q9DCJ7	Q9DCJ7 gallus gall

## ALIGNMENTS

RESULT 1	Q659F2	PRELIMINARY;	PRT;	531 AA.
ID	Q659F2			
AC	Q659F2			
DT	25-OCT-2004 (TrEMBLrel. 28, Created)			
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)			
DE	Hypothetical protein DKFZp434F053 (Fragment).			
GN	Name=DKFZp434F053;			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Testis;			
RG	The German CDNA Consortium;			
RA	Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,			
RA	Pobo G., Han M., Wiemann S.;			
RL	Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AL10280; CAH56406.1; -.			
KW	Hypothetical protein.			
FT	NON_TER			
FT	SEQUENCE 531 AA; 57158 MW; FEEDBC662369027B CRC64;			
Query Match	80.2%;	Score 264;	DB 2;	Length 531;
Best Local Similarity	82.8%;	Pred. No. 2.5e-23;		
Matches	48;	Conservative	0;	Mismatches 10; Indels 0; Gaps 0;
Qy	1 YPVRCLLPATGPCKARIRWYFVASVGQCNRFVYGCGRGNANFASBQECMSSCGGS 58			
Db	2 YPVRCLLPATGPCKARIRWYFVASVGQCNRFVYGCGRGNANFASBQECMSSCGGS 59			
RESULT 2	Q6ZNM1	PRELIMINARY;	PRT;	659 AA.
ID	Q6ZNM1			
AC	Q6ZNM1			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DE	FLJ00259 protein (Fragment).			
GN	Name=FLJ00259;			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RA	Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;			
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.			
DR	EMBL: AK131073; BAC85123.1; -.			

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DR HSSP: 016019: 1AAP.
DR GO: 0004867: F-serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003598; IG_c2.
DR InterPro: IPR003596; IG_v.
DR InterPro: IPR010909; PLAC.
DR InterPro: IPR002223; Proc_Inh_Kunz-m.
DR Pfam: PF00047; IG. 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00759; BASICTRASE.
DR ProDom: PD000222; Proc_Inh_Kunz-m; 1.
DR SMART: SM00409; IG_3.
DR SMART: SM00408; IGc2; 3.
DR SMART: SM00406; IGv; 3.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR PROSITE: PS50835; IG_LIKE; 3.
DR PROSITE: PS50900; PLAC; 1.
DR Non_TER 1
SQ SEQUENCE 659 AA; 70274 MW; 50FPA993B844C092 CRC64;

Query Match 80.2%; Score 264; DB 2; Length 659;
Best Local Similarity 82.8%; Pred. No. 3,1e-23;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 YPVRCILPPATGPCARIRIRWFVSVGQCNRFFVYGGCGGNANNFASDEQCMSSCGGS 58
Db 133 YPVRCILPPSAHSCADMARWYFVSVGQCNRFFWYGCGHGNANNFASDEQCMSSCGGS 188

RESULT 3
Q72681 PRELIMINARY; PRT; 660 AA.
ID Q72681;
AC Q72681;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp79D0163 (Fragment).
GN Name=DKFZp79D0163;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA The German cDNA Consortium;
RA Wambute R., Heubner D., Mewes H.W., Weil B., Amid C., Oanger A.,
RA Fobo G., Han M., Wiemann S.;
RA Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL: BX53757; CAD97826.1; -.
DR HSSP: Q16019: 1AAP.
DR GO: 0004867: F-serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003598; IG_c2.
DR InterPro: IPR010909; PLAC.
DR InterPro: IPR002223; Proc_Inh_Kunz-m.
DR Pfam: PF00047; IG. 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR ProDom: PD000222; Proc_Inh_Kunz-m; 1.
DR SMART: SM00408; IGc2; 3.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR PROSITE: PS50835; IG_LIKE; 3.
DR PROSITE: PS50900; PLAC; 1.
DR Hypothetical protein.
DR Non_TER 1
SQ SEQUENCE 660 AA; 70374 MW; A6D5B1C50CBB815 CRC64;
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Query Match 80.2%; Score 264; DB 2; Length 660;
Best Local Similarity 82.8%; Pred. No. 3,1e-23;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 YPVRCILPPATGPCARIRIRWFVSVGQCNRFFVYGGCGGNANNFASDEQCMSSCGGS 58
Db 133 YPVRCILPPSAHSCADMARWYFVSVGQCNRFFWYGCGHGNANNFASDEQCMSSCGGS 189

RESULT 4
O95428 PRELIMINARY; PRT; 1235 AA.
ID O95428;
AC O95428;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rowen L., Madan A., Qin S., Abbasi N., Dors M., Ratcliffe A.,
RA Madan A., Dickhoff R., Shaffer T., James R., Lasky S., Hood L.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL: AF109907; AAC97963.1; -.
DR HSSP: P1211; 1KTH.
DR Genew: HGNC:15262; PAPLN.
DR GO: 0004867: F-serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR010294; ADMN_spacer1; 1.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003598; IG_c2.
DR InterPro: IPR010909; PLAC.
DR InterPro: IPR002223; Proc_Inh_Kunz-m.
DR InterPro: IPR000884; TSP1.
DR Pfam: PF05986; ADMN_spacer1; 1.
DR Pfam: PF00047; IG. 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR Pfam: PF00090; TSP_1; 5.
DR PRINTS: PR00759; BASICTRASE.
DR ProDom: PD000222; Proc_Inh_Kunz-m; 1.
DR SMART: SM00408; IGc2; 3.
DR SMART: SM00131; KU; 1.
DR SMART: SM00209; TSP1; 5.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR PROSITE: PS50835; IG_LIKE; 3.
DR PROSITE: PS50900; PLAC; 1.
DR PROSITE: PS5092; TSP1; 5.
DR Hypothetical protein.
DR Non_TER 1
SQ SEQUENCE 1235 AA; 133476 MW; A0B44CCE4F38E350 CRC64;

Query Match 80.2%; Score 264; DB 2; Length 1235;
Best Local Similarity 82.8%; Pred. No. 5,6e-23;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 YPVRCILPPATGPCARIRIRWFVSVGQCNRFFVYGGCGGNANNFASDEQCMSSCGGS 58
Db 688 YPVRCILPPSAHSCADMARWYFVSVGQCNRFFWYGCGHGNANNFASDEQCMSSCGGS 745

RESULT 5
O9EPX2 PRELIMINARY; PRT; 1280 AA.
ID O9EPX2;
AC O9EPX2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Papilin.
GN Name=Paplin;
OS Mus musculus (Mouse).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CD-1;  
 RX MEDLINE=20530499; Pubmed=11076767;  
 RA Kramarova I.A., Kawaguchi N., Nelson R.E., Fessler J.I., Chen Y.,  
 RA Stenson A.L., Prockop D.J., Fessler J.H., Ackley B.D.,  
 RT "Papilin in development: a pericellular protein with a homology to the  
 RT ADAMTS metalloproteinases."  
 RL Development 127:5475-5485(2000).  
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
 DR EMBL: AF114171; AAC41980.1; -  
 DR HSSP: PL2111; 1KTH.  
 DR MSD; MG12386139; Papln.  
 DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
 DR InterPro: IPR010294; ADAM\_spacer1.  
 DR InterPro: IPR000183; Decarboxylase2.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003598; IG C2.  
 DR InterPro: IPR010909; PLAC.  
 DR InterPro: IPR002223; Prot\_Inh\_Kunz-m.  
 DR InterPro: IPR000884; TSPI.  
 DR Pfam: PF05986; ADAM\_spacer1; 1.  
 DR Pfam: PF00047; IG; 1.  
 DR Pfam: PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR PRODOM; PD000222; Prot\_Inh\_Kunz-m; 1.  
 DR SMART; SM00408; IGc2; 3.  
 DR SMART; SM00131; KU; 1.  
 DR SMART; SM00209; TSPI; 5.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 DR PROSITE; PS00879; ODR\_DC\_2\_2; UNKNOWN\_1.  
 DR PROSITE; PS50900; PLAC\_1\_1; UNKNOWN\_1.  
 DR PROSITE; PS50092; TSPI; 5.  
 SQ SEQUENCE 1280 AA; 138823 MW; AE287705B561AF30 CRC64;  
 Query Match 74.8%; Score 246; DB 2; Length 1280;  
 Best Local Similarity 75.4%; Pred. No. 8.5e-21;  
 Matches 43; Conservative 4; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 YPVRCILPPATGPGCKARIINWYFVASYGQCNRRFYGGCGNANNFASGEQCMSSCG 57  
 DB 746 YPVRCILPPASQSGCDMAARWYFVASYGRGNRRFYGGCGNANNFASGEQCMNTCRG 802  
 RESULT 6  
 BPTI\_BOVIN STANDARD; PRT; 100 AA.  
 ID BPTI\_BOVIN  
 AC P00974;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Pancreatic trypsin inhibitor precursor (Basic protease inhibitor)  
 DE (BPTI) (BPTI) (aprotinin).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87283904; Pubmed=2441071;  
 RA Creighton T.E., Charles I.G.;  
 RT "Sequences of the genes and polypeptide precursors for two bovine  
 RT protease inhibitors."  
 RL J. Mol. Biol. 194:11-22(1987).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=88295740; Pubmed=2456884;  
 RA Creighton T.E., Charles I.G.;  
 RT "Biosynthesis, processing, and evolution of bovine pancreatic trypsin  
 RT inhibitor."  
 RL Cold Spring Harb. Symp. Quant. Biol. 52:511-519(1987).  
 RN [3]  
 RP SEQUENCE OF 34-97 FROM N.A.  
 RX MEDLINE=86158754; Pubmed=2420326;  
 RA Kingston I.B., Anderson S.;  
 RT "Sequences encoding two trypsin inhibitors occur in strikingly similar  
 RT genomic environments."  
 RL Biochem. J. 233:443-450(1986).  
 RN [4]  
 RP SEQUENCE OF 34-97 FROM N.A.  
 RX MEDLINE=84070725; Pubmed=6580617;  
 RA Anderson S., Kingston I.B.;  
 RT "Isolation of a genomic clone for bovine pancreatic trypsin inhibitor  
 RT by using a unique-sequence synthetic DNA probe."  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:6838-6842(1983).  
 RN [5]  
 RP SEQUENCE OF 36-93, AND DISULFIDE BONDS.  
 RX MEDLINE=66083012; Pubmed=5860161;  
 RA Kassel B., Laekowski M.;  
 RT "The basic trypsin inhibitor of bovine pancreas. V. The disulfide  
 RT linkages."  
 RL Biochem. Biophys. Res. Commun. 20:463-468(1965).  
 RN [6]  
 RP SEQUENCE OF 36-93, AND DISULFIDE BONDS.  
 RX MEDLINE=66171231; Pubmed=5296424;  
 RA Anderer F.A., Horne S.;  
 RT "The disulfide linkages in kallikrein inactivator of bovine lung."  
 RL J. Biol. Chem. 241:1568-1572(1966).  
 RN [7]  
 RP SEQUENCE OF 36-93, AND DISULFIDE BONDS.  
 RX MEDLINE=68012003; Pubmed=6053284;  
 RA Chauvet J., Acher R.;  
 RT "Covalent structure of a polypeptide inhibitor of trypsin (Kunitz and  
 RT Northrop inhibitor)."  
 RL Bull. Soc. Chim. Biol. 49:985-1000(1967).  
 RN [8]  
 RP SEQUENCE OF 36-93.  
 RA Dlouha V., Pospisilova D., Meloun B., Sorm F.;  
 RT "Sequence of residues 18-20 in pancreatic trypsin inhibitor."  
 RL Collect. Czech. Chem. Commun. 33:1363-1365(1968).  
 RN [9]  
 RP SEQUENCE OF 36-81.  
 RC TISSUE=Adrenal chromaffin;  
 RX MEDLINE=90211226; Pubmed=2322242;  
 RA Lewis R.V., Ray P., Coghill R., Kruggel W.;  
 RT "Presence of pancreatic trypsin inhibitor in adrenal medullary  
 RT chromaffin cells."  
 RL Biochem. Biophys. Res. Commun. 167:543-547(1990).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).  
 RA Deisenhofer J., Steigemann W.;  
 RT "Crystallographic refinement of the structure of bovine pancreatic  
 RT trypsin inhibitor at 1.5-A resolution."  
 RL Acta Crystallogr. B 31:238-250(1975).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=70255230; Pubmed=5447861;  
 RA Huber R., Kukla D., Ruhlmann A., Epp O., Formanek H.;  
 RT "The basic trypsin inhibitor of bovine pancreas. I. Structure analysis  
 RT and conformation of the polypeptide chain."  
 RL Naturwissenschaften 57:389-392(1970).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT GLY-70.  
 RX MEDLINE=91332906; Pubmed=1714504;  
 RA Housset D., Kim K.-S., Fuchs J., Woodward C., Wlodawer A.;  
 RT "Crystal structure of a Y35G mutant of bovine pancreatic trypsin  
 RT inhibitor."  
 RL J. Mol. Biol. 220:757-770(1991).

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RN [13]
RP STRUCTURE BY NMR.
RX MEDLINE=9302116; PubMed=1383552;
RA Berndt K.D., Guntert P., Ordonez L.P.M., Wuehrich K.;
RT "Determination of a high-quality nuclear magnetic resonance solution
RT structure of the bovine pancreatic trypsin inhibitor and comparison
RT with three crystal structures."
RL J. Mol. Biol. 227:757-775(1992).
CC -1- FUNCTION: Inhibits trypsin, kallikrein, chymotrypsin, and plasmin.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PHARMACEUTICAL: Available under the name Traesylol (Mile). Used for
CC inhibiting coagulation so as to reduce blood loss during bypass
CC surgery.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- DATABASE: NAME=Traesylol; NOTE=Clinical information on Traesylol;
CC WWW="http://www.traesylol.com/".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M20934; AAD13685.1; -.
DR EMBL; M20930; AAD13685.1; JOINED.
DR EMBL; M20932; AAD13685.1; JOINED.
DR EMBL; X03365; CAA27062.1; ALT_SEQ.
DR EMBL; X03365; CAA27062.1; -.
DR EMBL; X05274; CAA28886.1; -.
DR FIR; S00277; TIBO.
DR PDB; 1AAL; X-ray; A/B=36-93.
DR PDB; 1B0C; X-ray; A/B/C/D/E=36-93.
DR PDB; 1BHC; X-ray; A/B/C/D/E/F/G/H/I/J=36-93.
DR PDB; 1BPI; X-ray; @=36-93.
DR PDB; 1BRB; X-ray; I=-.
DR PDB; 1BRH; X-ray; P/Q=36-93.
DR PDB; 1BT1; X-ray; @=36-93.
DR PDB; 1B25; X-ray; A/B/C/D/E=36-93.
DR PDB; 1B2X; X-ray; I=36-93.
DR PDB; 1C6W; X-ray; D/I=36-93.
DR PDB; 1C07; X-ray; I=2-100.
DR PDB; 1D0D; X-ray; B=36-93.
DR PDB; 1EAM; X-ray; B/D=36-93.
DR PDB; 1EJM; X-ray; B/D/F=36-93.
DR PDB; 1F5R; X-ray; I=36-100.
DR PDB; 1F7Z; X-ray; I=36-100.
DR PDB; 1FAK; X-ray; I=-.
DR PDB; 1FAN; X-ray; @=36-93.
DR PDB; 1FY8; X-ray; I=36-93.
DR PDB; 1G6X; X-ray; A=36-93.
DR PDB; 1JY8; NMR; A=36-93.
DR PDB; 1JY9; NMR; A/B=49-74.
DR PDB; 1K09; NMR; A/B=49-74.
DR PDB; 1K6U; X-ray; A=36-93.
DR PDB; 1LD5; NMR; A=36-93.
DR PDB; 1LD6; NMR; A=36-93.
DR PDB; 1MTN; X-ray; D/H=36-93.
DR PDB; 1NAG; X-ray; @=36-93.
DR PDB; 1OAS; NMR; 5=36-93.
DR PDB; 1OA6; NMR; 5=36-93.
DR PDB; 1PTT; NMR; @=36-93.
DR PDB; 1OLO; X-ray; A=36-93.
DR PDB; 1TPA; X-ray; I=36-93.
DR PDB; 1UUA; NMR; A=38-93.
DR PDB; 1UUB; NMR; A=38-93.
DR PDB; 2HEX; X-ray; A/B/C/D/E=36-93.
DR PDB; 2KX1; X-ray; I=36-93.
DR PDB; 2PTC; X-ray; I=36-93.
DR PDB; 2TGP; X-ray; I=36-93.
DR PDB; 2TPI; X-ray; I=35-93.

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DR PDB; 3BTD; X-ray; I=36-93.
DR PDB; 3BTE; X-ray; I=36-93.
DR PDB; 3BTF; X-ray; I=36-93.
DR PDB; 3BTG; X-ray; I=36-93.
DR PDB; 3BTH; X-ray; I=36-93.
DR PDB; 3BTM; X-ray; I=36-93.
DR PDB; 3BTK; X-ray; I=36-93.
DR PDB; 3BTL; X-ray; I=36-93.
DR PDB; 3BTP; X-ray; I=36-93.
DR PDB; 3BTW; X-ray; I=36-93.
DR PDB; 3BTX; X-ray; I=36-93.
DR PDB; 3BTY; X-ray; I=36-93.
DR PDB; 3BTZ; X-ray; I=36-93.
DR PDB; 3TCK; X-ray; I=36-100.
DR PDB; 3TPI; X-ray; I=36-93.
DR PDB; 4PT1; X-ray; @=36-93.
DR PDB; 4PTI; X-ray; I=36-93.
DR PDB; 5PT1; X-ray; @=36-93.
DR PDB; 6PT1; X-ray; @=36-93.
DR PDB; 7PT1; X-ray; @=36-93.
DR PDB; 8PT1; X-ray; @=36-93.
DR PDB; 9PT1; X-ray; @=36-92.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPRASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR 3D-structure; Direct protein sequencing; Pharmaceutical;
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 21 Potential.
FT PROPEP 22 35
FT CHAIN 36 93 Pancreatic trypsin inhibitor.
FT PROPEP 94 100
Query Match 58.4%; Score 192; DB 1; Length 100;
Best Local Similarity 57.9%; Pred. No. 2.3e-15;
Matches 33; Conservative 7; Mismatches 17; Indels 0; Gaps 0;
QY 2 PVRCLLPPTGPGCKARIIRWYFVASVGCCNRFVYGGCGRGNANPFASDEGCMSSCGGS 58
Db 37 PDCLEPPTGPGCKARIIRYFNARAGLCQTFVYGGCGAKRNFASDEGCMRTCGA 93
RESULT 7
ID 07M311 PRELIMINARY; PRT; 59 AA.
AC 07M311
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Isoprotinlin G1.
OS Bos indicus x Bos taurus (hybrid cattle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=30522;
RN [1]
RP MEDLINE=88221840; PubMed=2453200;
RA Stekman U., Wenzel H.R., Schroeder W., Tschesche H.;
RT "Characterization and sequence determination of six aproctinin
RT homologues from bovine lungs."
RL Biol. Chem. Hoppe-Seyler 359:157-163(1988).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; S00371; S00371.
DR HSSP; P00974; 1BPT.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPRASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

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DR PROSITE, PSS0279; BPTI\_KUNITZ\_2; 1.  
SQ SEQUENCE 59 AA; 6591 MW; B983C93192BBA418 CRC64;  
Query Match 57.8%; Score 190; DB 2; Length 59;  
Best Local Similarity 56.1%; Pred. No. 2.3e-15; Indels 0; Gaps 0;  
Matches 32; Conservative 9; Mismatches 16; Indels 0; Gaps 0;  
QY 2 PVRCLEPPATGPKARIIRWYFVASVGOQNRFFVYGGCRGNANFPASEQECSSCGGS 58  
3 PDCLEPPYTGPKAMIRYFYNAKAGLCQPFYGGCRASNPFKAEQECRTCGGA 59  
ID Q7M312 PRELIMINARY; PRT; 58 AA.  
AC Q7M312;  
DT 01-MAR-2004 (TEMBLrel. 26, Created)  
DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
DE Isoaprotinin G2.  
OS Bos indicus x Bos taurus (hybrid cattle).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OC NCBI\_TaxID=30522;  
OX NCBI\_TaxID=30522;  
RX MEDLINE=88221840; Pubmed=2453200;  
RA Stekamm J., Wenzel H.R., Schroeder W., Techesche H.;  
RT "Characterization and sequence determination of six aprotinin  
homologues from bovine lungs."  
RL Biol. Chem. Hoppe-Seyler 369:157-163 (1988).  
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
DR HSSP; P00974; 1BPT.  
DR GO; GO:0004667; F:serine-type endopeptidase inhibitor activity; IEA.  
DR InterPro; IPR002223; Prot. Inh. Kunz-m.  
DR Pfam; PF00014; Kunitz\_BPTI; 1.  
DR PRINTS; PR00759; BASICTPASE.  
DR ProDom; PD000222; Prot. Inh. Kunz-m; 1.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
DR PROSITE; PSS0279; BPTI\_KUNITZ\_2; 1.  
SQ SEQUENCE 58 AA; 6532 MW; B858E6092EA1518 CRC64;  
Query Match 57.1%; Score 188; DB 2; Length 58;  
Best Local Similarity 56.1%; Pred. No. 4e-15; Indels 0; Gaps 0;  
Matches 32; Conservative 8; Mismatches 17; Indels 0; Gaps 0;  
QY 2 PVRCLEPPATGPKARIIRWYFVASVGOQNRFFVYGGCRGNANFPASEQECSSCGGS 58  
3 PDCLEPPYTGPKAMIRYFYNAKAGLCQPFYGGCRASNPFKAEQECRTCGGA 58  
ID Q9GQNI PRELIMINARY; PRT; 984 AA.  
AC Q9GQNI;  
DT 01-MAR-2001 (TEMBLrel. 16, Created)  
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  
DE Peptidylglycine alpha-amidating monooxygenase.  
GN Name=PAM;  
OS Calliacis parasitica (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;  
OC Nymphaeae; Hornichidae; Calliacis.  
OC NCBI\_TaxID=6114;  
OX NCBI\_TaxID=6114;  
RX SEQUENCE FROM N.A.  
RA Williamson M., Hauser F., Grimmelikhuijzen C.J.P.;  
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
DR EMBL; AF221986; AAG44251.1; -.  
DR HSSP; P12111; 1KNT.

DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005507; F:copper ion binding; IEA.  
DR GO; GO:0004504; F:peptidylglycine monooxygenase activity; IEA.  
DR GO; GO:0004667; F:serine-type endopeptidase inhibitor activity; IEA.  
DR GO; GO:0006168; F:peptide metabolism; IEA.  
DR InterPro; IPR011044; Amino DH B\_Like.  
DR InterPro; IPR001258; Cu2\_monooxygenase.  
DR InterPro; IPR000720; Pamonoxgenase.  
DR InterPro; IPR008977; PHM\_PNGase F.  
DR InterPro; IPR002223; Prot. Inh. Kunz-m.  
DR Pfam; PF01082; Cu2\_monooxygen; 1.  
DR Pfam; PF03712; Cu2\_monoox C; 1.  
DR Pfam; PF00014; Kunitz\_BPTI; 1.  
DR Pfam; PF01436; NHL; 5.  
DR PRINTS; PR00759; BASICTPASE.  
DR PRINTS; PR00790; PAMONOXGNASE.  
DR SMART; SM00131; KU; 1.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
DR PROSITE; PSS0279; BPTI\_KUNITZ\_2; 1.  
DR PROSITE; PS00084; CU2\_MONOOXYGENASE\_1; 1.  
KW Monooxygenase.  
SQ SEQUENCE 984 AA; 110265 MW; 4C24E4BCB3B480D CRC64;  
Query Match 56.5%; Score 186; DB 2; Length 984;  
Best Local Similarity 54.5%; Pred. No. 1.1e-13; Indels 0; Gaps 0;  
Matches 30; Conservative 8; Mismatches 17; Indels 0; Gaps 0;  
QY 1 YVRCLEPPATGPKARIIRWYFVASVGOQNRFFVYGGCRGNANFPASEQECSSCG 55  
726 PFAFCLEHDTGFCRAMPRWYFADAKARSTRTFYGGCGNENFPASKRECEAKC 780  
ID Q9GQNI PRELIMINARY; PRT; 984 AA.  
AC Q9GQNI;  
DT 01-MAR-2001 (TEMBLrel. 16, Created)  
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)  
DE Peptidylglycine alpha-amidating monooxygenase.  
GN Name=PAM;  
OS Calliacis parasitica (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;  
OC Nymphaeae; Hornichidae; Calliacis.  
OC NCBI\_TaxID=6114;  
OX NCBI\_TaxID=6114;  
RX SEQUENCE FROM N.A.  
RA Williamson M., Hauser F., Grimmelikhuijzen C.J.P.;  
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
DR EMBL; AF221985; AAG44250.1; -.  
DR HSSP; P12111; 1KNT.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005507; F:copper ion binding; IEA.  
DR GO; GO:0004504; F:peptidylglycine monooxygenase activity; IEA.  
DR GO; GO:0004667; F:serine-type endopeptidase inhibitor activity; IEA.  
DR GO; GO:0006168; F:peptide metabolism; IEA.  
DR InterPro; IPR011044; Amino DH B\_Like.  
DR InterPro; IPR001258; Cu2\_monooxygenase.  
DR InterPro; IPR000720; Pamonoxgenase.  
DR InterPro; IPR008977; PHM\_PNGase F.  
DR InterPro; IPR002223; Prot. Inh. Kunz-m.  
DR Pfam; PF01082; Cu2\_monooxygen; 1.  
DR Pfam; PF03712; Cu2\_monoox C; 1.  
DR Pfam; PF00014; Kunitz\_BPTI; 1.  
DR Pfam; PF01436; NHL; 5.  
DR PRINTS; PR00759; BASICTPASE.  
DR PRINTS; PR00790; PAMONOXGNASE.  
DR ProDom; PD000222; Prot. Inh. Kunz-m; 1.  
DR SMART; SM00131; KU; 1.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.



```
DR PROSITE: PSS0279; BPTI_KUNITZ_2; 1.
DR PROSITE: PSS0084; CUG2_MONOOXYGENASE_1; 1.
KW Monooxygenase.
SQ SEQUENCE 984 AA; 110266 MW; 7AFE2D1B74B78BC CRC64;

Query Match
Best Local Similarity 54.5%; Score 186; DB 2; Length 984;
Matches 30; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

OY 1 YFVRCILPPATGPKARIRRMVFVAVSGQCNRFVYGGCGGNANNPASBECMSSC 55
Db 726 FPAFCWLEHDTGFCRAAMPFWFDADAKARCTRTIYGGCGGNENNFASKCEAKC 780

RESULT 11
O6IND9 PRELIMINARY; PRT; 327 AA.
AC O6IND9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE MGCB165 protein (Fragment).
GN Name=MGCB165;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxId=8355;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feigold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Matsushima K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant J.L., Scheetz T.E.,
RA Brownstein M.U., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Munry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
[3]
RN SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RC Klein S., Strausberg R.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL: BC072344; AAH72344.1; -.
DR HSSP: Q16019; IAP.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0030414; F:protease inhibitor activity; IEA.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO: GO:0007596; P:blood coagulation; IEA.
```

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DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR InterPro: IPR008286; TPPI.
DR Pfam: PF00014; Kunitz_BPTI_3.
DR PIRSF: PIRSF001620; TPPI_1.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot_Inh_Kunz-m; 3.
DR SMART: SM00131; KU; 1.
DR PROSITE: PSS0280; BPTI_KUNITZ_1; 2.
DR PROSITE: PSS0279; BPTI_KUNITZ_2; 3.
FT NON TER 1
SQ SEQUENCE 327 AA; 35951 MW; 2BFE6FA75DAB0497 CRC64;

Query Match
Best Local Similarity 56.2%; Score 185; DB 2; Length 327;
Matches 29; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

OY 1 YFVRCILPPATGPKARIRRMVFVAVSGQCNRFVYGGCGGNANNPASBECMSSC 57
Db 197 YSEYCAASLSTGPCASFSRWYDRTTSGCATFIYGGCGGNANNTLSDDDCVKNCVG 253

RESULT 12
IBPS_BOVIN STANDARD; PRT; 60 AA.
AC P00975;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serum basic protease inhibitor (Serum BPI).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxId=9913;
[1]
RP SEQUENCE.
RX MEDLINE=81044408; PubMed=7428928; DOI=10.1016/0014-5793(80)80997-5;
RA Wachter E., Deppner K., Hochstrasser K., Lempert K., Geiger R.,
RT "A new Kunitz-type inhibitor from bovine serum amino acid sequence
RT determination."
RL FEBS Lett. 119:58-62(1980).
CC -1- FUNCTION: This inhibitor has activity very similar to that of the
CC basic protease inhibitor from bovine tissues.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR: A01206; TIBOR.
DR HSSP: P00974; IBPI.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI_1.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot_Inh_Kunz-m; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PSS0280; BPTI_KUNITZ_1; 1.
DR PROSITE: PSS0279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Serine protease inhibitor.
FT SITE 17 18 Reactive bond.
FT DISULFID 7 57 By similarity.
FT DISULFID 16 40 By similarity.
FT DISULFID 32 53 By similarity.
SQ SEQUENCE 60 AA; 6647 MW; B9953EBAACF1A4E6 CRC64;

Query Match
Best Local Similarity 55.9%; Score 184; DB 1; Length 60;
Matches 31; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

OY 2 YFVRCILPPATGPKARIRRMVFVAVSGQCNRFVYGGCGGNANNPASBECMSSC 58
Db 4 YDFCLPEPTGPKAMIRYFNAYAGCETFVYGGCGRAKSNFYSADCKRTCGA 60

RESULT 13
BPT2_BOVIN STANDARD; PRT; 100 AA.
```

AC P04815;1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 10, Last sequence update)  
DT 01-MAR-1989 (Rel. 14, Last annotation update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Spleen trypsin inhibitor I precursor (SI-I) [Contains: Spleen trypsin  
DE inhibitor II (SI-II); Spleen trypsin inhibitor III (SI-III)].  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Kumlantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87283904; PubMed=2441071;  
RA Creighton T.B., Charles I.G.;  
RT "Sequences of the genes and polypeptide precursors for two bovine  
RT protease inhibitors."  
RL J. Mol. Biol. 194:11-22(1987).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88295740; PubMed=2456884;  
RA Creighton T.B., Charles I.G.;  
RT "Biosynthesis, processing, and evolution of bovine pancreatic trypsin  
RT inhibitor."  
RL Cold Spring Harb. Symp. Quant. Biol. 52:511-519(1987).  
RN [3]  
RP SEQUENCE OF 34-97 FROM N.A.  
RX MEDLINE=86158754; PubMed=2420326;  
RA Kingston I.B., Anderson S.;  
RT "Sequences encoding two trypsin inhibitors occur in strikingly similar  
RT genomic environments."  
RL Biochem. J. 233:443-450(1986).  
RN [4]  
RP SEQUENCE OF 34-99.  
RX MEDLINE=89076531; PubMed=2462435;  
RA Fioretti E., Angeletti M., Fiorucci L., Barra D., Bosca F., Ascoli F.;  
RT "Aprotinin-like isoinhibitors in bovine organs."  
RL Biol. Chem. Hoppe-Seyler 369:37-42(1988).  
RN [5]  
RP SEQUENCE OF 34-99.  
RX MEDLINE=88007630; PubMed=3654647;  
RA Barra D., Stimmaco M., Bosca F., Fioretti E., Angeletti M., Ascoli F.;  
RT "Primary structure of a protease isoinhibitor from bovine spleen. A  
RT possible intermediate in the processing of the primary gene product."  
RL J. Biol. Chem. 262:13916-13919(1987).  
RN [6]  
RP SEQUENCE OF 36-93.  
RC TISSUE=Spleen;  
RX MEDLINE=86008178; PubMed=2413011;  
RA Fioretti E., Iacopino G., Angeletti M., Barra D., Bosca F., Ascoli F.;  
RT "Primary structure and antiproteolytic activity of a Kunitz-type  
RT inhibitor from bovine spleen."  
RL J. Biol. Chem. 260:11451-11455(1985).  
RN [7]  
RP SEQUENCE OF 36-97.  
RC TISSUE=Spleen;  
RX MEDLINE=91096258; PubMed=1986787; DOI=10.1016/0167-4838(91)90231-N;  
RA Barra D., Fioretti E., Angeletti M., Maras B., Bosca F., Ascoli F.;  
RT "Proteinase isoinhibitors from bovine spleen: primary structure of an  
RT intermediate in the processing of the precursor."  
RL Biochim. Biophys. Acta 1076:143-147(1991).  
RN [8]  
RP SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
CC  
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CC -----

DR	EMBL; M20935; AAA51418.1; -	JOINED.
DR	EMBL; M20931; AAA51418.1; -	JOINED.
DR	EMBL; M20933; AAA51418.1; -	JOINED.
DR	EMBL; X05275; CAA28887.1; -	
DR	EMBL; X06685; CAA29881.1; -	
DR	EMBL; X03366; CAA27064.1; ALU_Seq.	
DR	EMBL; X03366; CAA27065.1; -	
DR	PIR; S00274; TIBOSP.	
DR	HSSP; P00974; 1BPI.	
DR	InterPro; IPRO02223; Prot Inh_Kunz-m.	
DR	Pfam; PF00014; Kunitz_Bpt1.	
DR	PRINTS; PR00759; BASICPTASE.	
DR	ProDom; PD000222; Prot_Inh_Kunz-m; 1.	
DR	SMART; SM00131; KU; 1.	
DR	PROSITE; PS00280; BPT1_KUNITZ_1; 1.	
DR	PROSITE; PS0279; BPT1_KUNITZ_2; 1.	
KM	Direct protein sequencing; Serine protease inhibitor; Signal.	
FT	SIGNAL	1 21
FT	PROPEP	22 33
FT	CHAIN	34 99
FT	CHAIN	36 93
FT	CHAIN	36 97
FT	DOMAIN	40 90
FT	SITE	50 51
FT	DISULFID	40 90
FT	DISULFID	49 73
FT	DISULFID	65 86
QC	SEQUENCE	100 AA; 10843 MW; 39069734B8ACFAE3 CRC64;

Query Match	55.9%	Score 184	DB 1	length 100
Best Local Similarity	52.6%	Pred. No. 2.1e-14		
Matches 30	Conservative 11	Mismatches 16	Indels 0	Gaps 0

Qy 2 PVRCILIPATGDCKARIIRWYPASVGCNRPVYGGCGKANNFASBQECMSSCGGS 58  
Db 37 PDFCLRPYPYTGCKAKMIRYPYAKAGPFCETFFVYGGCKAKSNFRSAEDMCRPTCGGA 93

## RESULT 14

ID	Q7ZZT3	PRELIMINARY;	PRT;	82 AA.
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DT 01-JUN-2003 (TREMBlere). 24, Created

DT 01-OCT-2003 (Tremblay, 25, Last annotation update)

GN Name=apbb;

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Cyprinidae; Danio.

RN	[1]
----	-----

RA Groth C., Lardelli M.;

CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

DR HSSP; Q16019; 1AAP.

DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.

DR Pfam; PF00014; Kunitz\_BPTI; 1.

DR ProDom; PD000222; Prot\_Inh\_Kunz-m; 1.

DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.

FT	NON_TER	1	1
FE	NOV_FET	00	00

SQ SEQUENCE 82 AA; 8874 MW; 0723D4AC6585B349 CRC64;

Query Match 53.8%; Score 177; DB 2; Length 82;

Best Local Similarity 53.7%; Pred. No. 1,2e-13;  
Matches 29; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 5 CLLPATPCKARIRMYFVASVGQCNRFVYGGCRGNANNFASBOECMSSCGS 58  
DB 22 CMAPASGFCXALPRMYFAVEKGRCSAFTFGCGGGRNNFSESEBXCMAVCSS 75

## RESULT 15

UPTI\_PIG STANDARD; PRT; 122 AA.  
AC 029100;  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Uterine plasmin/trypsin inhibitor precursor (UPTI).  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN (1)  
RP SEQUENCE FROM N.A., SEQUENCE OF 30-56, AND CHARACTERIZATION.  
RC TISSUE=Conceptus membrane, and Uterus;  
RX MEDLINE=95014140; PubMed=7929061;  
RA Stallings-Mann M.L., Burke M.G., Trout W.E., Roberts R.M.;  
RT "Purification, characterization, and cDNA cloning of a Kunitz-type  
proteinase inhibitor secreted by the porcine uterus.";  
J. Biol. Chem. 269:24090-24094(1994).  
RL -1- FUNCTION: Inhibitor of plasmin and trypsin. Also has a weak  
affinity for chymotrypsin. Could serve to neutralize the  
activities of one or more serine proteinases generated by the  
proliferating trophoblast during the formation of the noninvasive  
placenta.  
CC -1- TISSUE SPECIFICITY: Expressed only in the uterus and the  
endometrium.  
CC -1- DEVELOPMENTAL STAGE: Maximally expressed during pregnancy until  
day 30 after which levels decrease significantly.  
CC -1- INDUCTION: By progesterone.  
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
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DR EMBL, L14282; AAA62425.1; -.  
DR FIR; A55115; A55115.  
DR HSSP; P00974; 1K09.  
DR InterPro; IPR002223; ProtInh\_Kunz-m.  
DR Pfam; PF00014; Kunitz\_BPTI; 1.  
DR PRINTS; PR00759; BASICTPASE.  
DR PRODOM; PD000222; ProtInh\_Kunz-m; 1.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 1.  
KW Direct protein sequencing; Serine protease inhibitor; Signal.  
FT SIGNAL 1 20 Potential.  
FT PROPEP 21 29  
FT CHAIN 30 122 Uterine plasmin/trypsin inhibitor.  
FT DOMAIN 38 88 BPTI/Kunitz inhibitor.  
FT SITE 48 49 Reactive bond (By similarity).  
FT DISULFID 38 88 By similarity.  
FT DISULFID 47 71 By similarity.  
FT DISULFID 63 84 By similarity.  
FT CONFLICT 36 36 G -> A (in Ref. 1; AA sequence).  
FT CONFLICT 48 48 S -> R (in Ref. 1; AA sequence).  
FT CONFLICT 52 52 V -> I (in Ref. 1; AA sequence).  
FT CONFLICT 54 54 Y -> V (in Ref. 1; AA sequence).  
SQ SEQUENCE 122 AA; 13109 MW; B9BEFB3A6FB76CEC CRC64;

Query Match 52.9%; Score 174; DB 1; Length 122;

Best Local Similarity 51.9%; Pred. No. 4e-13;  
Matches 28; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 2 PYRCLLPATPCKARIRMYFVASVGQCNRFVYGGCRGNANNFASBOECMSSC 55  
DB 35 PGFCREPPYTGCSAHFVAFYFNATTTGLGQSFVYGGCRGKQNNFMDKXCLHTC 88

Search completed: August 25, 2005, 04:55:26  
Job time : 180 secs

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OM protein - protein search, using sw model

Run on: August 25, 2005, 04:49:39 ; Search time 162 Seconds  
(without alignments)  
140.197 Million cell updates/sec

Title: US-10-721-961-4  
Perfect score: 329  
Sequence: 1 YPVRCILPPATGPKARIIR.....RGNNANFASBOECSSCGS 58

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgnt2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep:\*  
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3: /cgnt2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgnt2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*  
5: /cgnt2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
6: /cgnt2\_6/ptodata/1/pubppa/PCTUS\_PUBCOMB.pep:\*  
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8: /cgnt2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep:\*  
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14: /cgnt2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*  
15: /cgnt2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*  
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18: /cgnt2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*  
19: /cgnt2\_6/ptodata/1/pubppa/US11\_PUBCOMB.pep:\*  
20: /cgnt2\_6/ptodata/1/pubppa/US11\_NEW\_PUB.pep:\*  
21: /cgnt2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep:\*  
22: /cgnt2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	100.0	58	16	US-10-721-961-4
2	326	99.1	58	16	US-10-721-961-5
3	314	95.4	58	16	US-10-721-961-7
4	314	95.4	58	16	US-10-721-961-34
5	291	88.4	58	16	US-10-721-961-6
6	291	88.4	58	16	US-10-721-961-33
7	264	80.2	58	16	US-10-721-961-1
8	264	80.2	111	16	US-10-721-961-32
9	264	80.2	1280	15	US-10-262-839-92
10	264	80.2	1311	14	US-10-103-377C-6
11	264	80.2	1311	16	US-10-391-364-91

12	246	74.8	1280	14	US-10-087-887-86	Sequence 86, Appl
13	193	58.7	57	8	US-08-896-322-5	Sequence 5, Appl1
14	193	58.7	57	14	US-10-252-967-5	Sequence 5, Appl1
15	192	58.4	58	9	US-09-234-874A-7	Sequence 7, Appl1
16	192	58.4	58	9	US-09-234-874A-108	Sequence 108, App
17	192	58.4	58	9	US-09-030-619-173	Sequence 173, App
18	192	58.4	58	9	US-09-912-609-61	Sequence 61, Appl1
19	192	58.4	58	9	US-09-113-244-2	Sequence 2, Appl1
20	192	58.4	58	9	US-09-781-988-44	Sequence 44, Appl1
21	192	58.4	58	10	US-09-234-873A-7	Sequence 7, Appl1
22	192	58.4	58	10	US-09-234-873A-108	Sequence 108, App
23	192	58.4	58	10	US-09-788-006-55	Sequence 55, Appl1
24	192	58.4	58	10	US-09-893-878-44	Sequence 44, Appl1
25	192	58.4	58	10	US-09-974-026-24	Sequence 24, Appl1
26	192	58.4	58	10	US-09-896-095-44	Sequence 44, Appl1
27	192	58.4	58	10	US-09-896-095-144	Sequence 144, App
28	192	58.4	58	10	US-09-896-095-181	Sequence 181, App
29	192	58.4	58	14	US-10-076-604-7	Sequence 7, Appl1
30	192	58.4	58	14	US-10-076-604-108	Sequence 108, App
31	192	58.4	58	14	US-10-167-351-38	Sequence 38, Appl1
32	192	58.4	58	14	US-10-038-722-6	Sequence 6, Appl1
33	192	58.4	58	14	US-10-038-722-87	Sequence 87, Appl1
34	192	58.4	58	14	US-10-038-722-124	Sequence 124, App
35	192	58.4	58	15	US-10-277-232-173	Sequence 173, App
36	192	58.4	58	15	US-10-126-685-44	Sequence 44, Appl1
37	192	58.4	58	15	US-10-115-134-1	Sequence 1, Appl1
38	192	58.4	58	15	US-10-115-134-38	Sequence 38, Appl1
39	192	58.4	58	15	US-10-277-233-173	Sequence 173, App
40	192	58.4	58	15	US-10-127-028-44	Sequence 44, Appl1
41	192	58.4	58	15	US-10-360-101-205	Sequence 205, App
42	192	58.4	58	15	US-10-126-544-44	Sequence 44, Appl1
43	192	58.4	58	15	US-10-456-986A-29	Sequence 29, Appl1
44	192	58.4	58	15	US-10-456-981-23	Sequence 23, Appl1
45	192	58.4	58	17	US-10-718-966-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-10-721-961-4  
; Sequence 4, Application US/10721961  
; Publication No. US20040152633A1  
; GENERAL INFORMATION:  
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.  
; APPLICANT: Jorgensen, Mariame U  
; APPLICANT: Jorgensen, Bang  
; APPLICANT: Olesen, Ole H  
; APPLICANT: Petersen, Lars C  
; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides  
; FILE REFERENCE: 6297.204-US  
; CURRENT APPLICATION NUMBER: US/10/721,961  
; CURRENT FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: US 60/303,180  
; PRIOR FILING DATE: 2001-07-05  
; PRIOR APPLICATION NUMBER: PCT/DK02/00372  
; PRIOR FILING DATE: 2002-05-31  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 58  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-721-961-4

Query Match 100.0%; Score 329; DB 16; Length 58;  
Best Local Similarity 100.0%; Pred. No. 5.6e-32;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 YPVRCILPPATGPKARIIRFVASVGCCNRFTVGGCGNANFASBOECSSCGS 58  
|||||

Db 1 YPVRCLLPATGPCKARIIRWYFVASVGQCNRFVYGGCGGNANNPASBQECMSSCGGS 58

## RESULT 2

US-10-721-961-5  
; Sequence 5, Application US/10721961  
; Publication No. US20040152633A1  
; GENERAL INFORMATION:  
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.  
; APPLICANT: Jorgensen, Marianne U  
; APPLICANT: Susanne, Bang  
; APPLICANT: Olesen, Ole H  
; APPLICANT: Petersen, Lars C  
; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides  
; FILE REFERENCE: 6297.204-US  
; CURRENT APPLICATION NUMBER: US/10/721,961  
; PRIOR FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: US 60/303,180  
; PRIOR FILING DATE: 2001-07-05  
; PRIOR APPLICATION NUMBER: PCT/DK02/00372  
; PRIOR FILING DATE: 2002-05-31  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 58  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-721-961-5

Query Match 99.1%; Score 326; DB 16; Length 58;  
Best Local Similarity 98.3%; Pred. No. 1.3e-31;  
Matches 57; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YPVRCLLPATGPCKARIIRWYFVASVGQCNRFVYGGCGGNANNPASBQECMSSCGGS 58  
Db 1 YPVRCLLPATGPCKARIIRWYFVASVGQCNRFVYGGCGGNANNPASBQECMSSCGGS 58

## RESULT 3

US-10-721-961-7  
; Sequence 7, Application US/10721961  
; Publication No. US20040152633A1  
; GENERAL INFORMATION:  
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.  
; APPLICANT: Jorgensen, Marianne U  
; APPLICANT: Susanne, Bang  
; APPLICANT: Olesen, Ole H  
; APPLICANT: Petersen, Lars C  
; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides  
; FILE REFERENCE: 6297.204-US  
; CURRENT APPLICATION NUMBER: US/10/721,961  
; PRIOR FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: US 60/303,180  
; PRIOR FILING DATE: 2001-07-05  
; PRIOR APPLICATION NUMBER: PCT/DK02/00372  
; PRIOR FILING DATE: 2002-05-31  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 58  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-721-961-7

Query Match 95.4%; Score 314; DB 16; Length 58;  
Best Local Similarity 94.8%; Pred. No. 3.6e-30;  
Matches 55; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YPVRCLLPATGPCKARIIRWYFVASVGQCNRFVYGGCGGNANNPASBQECMSSCGGS 58

Db 1 YPVRCLLPATGPCKARAARWYFVASVGQCNRFVYGGCGGNANNPASBQECMSSCGGS 58

## RESULT 4

US-10-721-961-34  
; Sequence 34, Application US/10721961  
; Publication No. US20040152633A1  
; GENERAL INFORMATION:  
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.  
; APPLICANT: Jorgensen, Marianne U  
; APPLICANT: Susanne, Bang  
; APPLICANT: Olesen, Ole H  
; APPLICANT: Petersen, Lars C  
; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides  
; FILE REFERENCE: 6297.204-US  
; CURRENT APPLICATION NUMBER: US/10/721,961  
; PRIOR FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: US 60/303,180  
; PRIOR FILING DATE: 2001-07-05  
; PRIOR APPLICATION NUMBER: PCT/DK02/00372  
; PRIOR FILING DATE: 2002-05-31  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 34  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Artificial  
; OTHER INFORMATION: Amino acid sequence of the 212L-HK118-2 fusion polypeptide  
US-10-721-961-34

Query Match 95.4%; Score 314; DB 16; Length 111;  
Best Local Similarity 94.8%; Pred. No. 6.6e-30;  
Matches 55; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YPVRCLLPATGPCKARAARWYFVASVGQCNRFVYGGCGGNANNPASBQECMSSCGGS 58  
Db 54 YPVRCLLPATGPCKARAARWYFVASVGQCNRFVYGGCGGNANNPASBQECMSSCGGS 111

## RESULT 5

US-10-721-961-6  
; Sequence 6, Application US/10721961  
; Publication No. US20040152633A1  
; GENERAL INFORMATION:  
; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.  
; APPLICANT: Jorgensen, Marianne U  
; APPLICANT: Susanne, Bang  
; APPLICANT: Olesen, Ole H  
; APPLICANT: Petersen, Lars C  
; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides  
; FILE REFERENCE: 6297.204-US  
; CURRENT APPLICATION NUMBER: US/10/721,961  
; PRIOR FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: US 60/303,180  
; PRIOR FILING DATE: 2001-07-05  
; PRIOR APPLICATION NUMBER: PCT/DK02/00372  
; PRIOR FILING DATE: 2002-05-31  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 58  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-721-961-6

Query Match 88.4%; Score 291; DB 16; Length 58;  
Best Local Similarity 89.7%; Pred. No. 2.1e-27;

Matches 52; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 YPVRCILPPATGCKARIIRWYFVASVGQCNRFVYGGCGGNANNFASSEQECMSSCGGS 58  
 DB 1 YPVRCILPPATGCKMAARWYFVASVGQCNRFWYGGCHGNANNFASSEQECMSSCGGS 58

RESULT 6  
 US-10-721-961-33  
 ; Sequence 33, Application US/10721961  
 ; Publication No. US20040152633A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.  
 ; APPLICANT: Jorgensen, Marianne U  
 ; APPLICANT: Susanne, Bang  
 ; APPLICANT: Olesen, Ole H  
 ; APPLICANT: Petersen, Lars C  
 ; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides  
 ; FILE REFERENCE: 6297.204-US  
 ; CURRENT APPLICATION NUMBER: US/10/721,961  
 ; PRIOR FILING DATE: 2003-11-25  
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859  
 ; PRIOR FILING DATE: 2001-05-31  
 ; PRIOR APPLICATION NUMBER: US 60/303,180  
 ; PRIOR FILING DATE: 2001-07-05,  
 ; PRIOR APPLICATION NUMBER: PCT/DK02/00372  
 ; PRIOR FILING DATE: 2002-05-31  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 33  
 ; LENGTH: 111  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Amino acid sequence of the 212L-HK18-1 fusion polypeptide  
 US-10-721-961-33

Query Match 88.4%; Score 291; DB 16; Length 111;  
 Best Local Similarity 89.7%; Pred. No. 3.8e-27;  
 Matches 52; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 YPVRCILPPATGCKARIIRWYFVASVGQCNRFVYGGCGGNANNFASSEQECMSSCGGS 58  
 DB 54 YPVRCILPPATGCKMAARWYFVASVGQCNRFWYGGCHGNANNFASSEQECMSSCGGS 111

RESULT 7  
 US-10-721-961-1  
 ; Sequence 1, Application US/10721961  
 ; Publication No. US20040152633A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.  
 ; APPLICANT: Jorgensen, Marianne U  
 ; APPLICANT: Susanne, Bang  
 ; APPLICANT: Olesen, Ole H  
 ; APPLICANT: Petersen, Lars C  
 ; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides  
 ; FILE REFERENCE: 6297.204-US  
 ; CURRENT APPLICATION NUMBER: US/10/721,961  
 ; PRIOR FILING DATE: 2003-11-25  
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859  
 ; PRIOR FILING DATE: 2001-05-31  
 ; PRIOR APPLICATION NUMBER: US 60/303,180  
 ; PRIOR FILING DATE: 2001-07-05  
 ; PRIOR APPLICATION NUMBER: PCT/DK02/00372  
 ; PRIOR FILING DATE: 2002-05-31  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 1  
 ; LENGTH: 58  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:

; OTHER INFORMATION: Amino acid sequence of human wild type HK1-18  
 US-10-721-961-1  
 Query Match 80.2%; Score 264; DB 16; Length 58;  
 Best Local Similarity 82.8%; Pred. No. 3.7e-24;  
 Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 YPVRCILPPATGCKARIIRWYFVASVGQCNRFVYGGCGGNANNFASSEQECMSSCGGS 58  
 DB 1 YPVRCILPPATGCKADMAARWYFVASVGQCNRFWYGGCHGNANNFASSEQECMSSCGGS 58  
 RESULT 8  
 US-10-721-961-32  
 ; Sequence 32, Application US/10721961  
 ; Publication No. US20040152633A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Novo Nordisk Pharmaceuticals, Inc.  
 ; APPLICANT: Jorgensen, Marianne U  
 ; APPLICANT: Susanne, Bang  
 ; APPLICANT: Olesen, Ole H  
 ; APPLICANT: Petersen, Lars C  
 ; TITLE OF INVENTION: Kunitz-Type Sequences and Polypeptides  
 ; FILE REFERENCE: 6297.204-US  
 ; CURRENT APPLICATION NUMBER: US/10/721,961  
 ; PRIOR FILING DATE: 2003-11-25  
 ; PRIOR APPLICATION NUMBER: Danish Application No. PA 2001 00859  
 ; PRIOR FILING DATE: 2001-05-31  
 ; PRIOR APPLICATION NUMBER: US 60/303,180  
 ; PRIOR FILING DATE: 2001-07-05  
 ; PRIOR APPLICATION NUMBER: PCT/DK02/00372  
 ; PRIOR FILING DATE: 2002-05-31  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 32  
 ; LENGTH: 111  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Amino acid sequence of the 212L-HK18 fusion polypeptide  
 US-10-721-961-32

Query Match 80.2%; Score 264; DB 16; Length 111;  
 Best Local Similarity 82.8%; Pred. No. 6.8e-24;  
 Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 YPVRCILPPATGCKARIIRWYFVASVGQCNRFVYGGCGGNANNFASSEQECMSSCGGS 58  
 DB 54 YPVRCILPPATGCKADMAARWYFVASVGQCNRFWYGGCHGNANNFASSEQECMSSCGGS 111  
 RESULT 9  
 US-10-262-839-92  
 ; Sequence 92, Application US/10262839  
 ; Publication No. US20040038877A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alsobrook, John  
 ; APPLICANT: Anderson, David W.,  
 ; APPLICANT: Boldog, Ferenc  
 ; APPLICANT: Burgess, Catherine  
 ; APPLICANT: Caterton, Elina  
 ; APPLICANT: Edinger, Shlomit  
 ; APPLICANT: Ellerman, Karen  
 ; APPLICANT: Gerlach, Valerie  
 ; APPLICANT: Gorman, Linda  
 ; APPLICANT: Guo, Xiaojia  
 ; APPLICANT: Ji, Weizhen  
 ; APPLICANT: Kekuda, Ramesh  
 ; APPLICANT: Leach, Martin  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Miller, Charles  
 ; APPLICANT: Patuturajan, Meera  
 ; APPLICANT: Reiger, Daniel

```

; APPLICANT: Rothenberg, Mark,
; APPLICANT: Shimkets, Richard,
; APPLICANT: Smithson, Glenda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Taupier, Raymond, Jr.,
; APPLICANT: Vernet, Corine,
; APPLICANT: Vose, Edward,
; APPLICANT: Zernhusen, Brian,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-462A
; CURRENT APPLICATION NUMBER: US/10/262,839
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/326,483
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/381,101
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/371,972
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/327,342
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/328,044
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/374,738
; PRIOR FILING DATE: 2002-04-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: CuroseqList version 0.1
; SEQ ID NO 92
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-262-839-92

Query Match      80.2%; Score 264; DB 15; Length 1280;
Best Local Similarity 82.8%; Pred. No. 6,7e-23;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy      1 YPVRCLLPATGPKARIRIRWYFVASVGQCNRFVYGGCGNANNFASBOECMSSCGGS 58
Db      752 YPVRCLLPASGSCADMARWTFVASVGQCNRFWYGCGHGNANNFASBOECMSSCGGS 809

RESULT 10
; US-10-103-377C-6
; Sequence 6, Application US/10103377C
; Publication No. US20030073098A1
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: 65577, A Human Matrix
; FILE REFERENCE: MP101-049PIRM
; CURRENT APPLICATION NUMBER: US/10/103,377C
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/278,347
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1311
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-103-377C-6

Query Match      80.2%; Score 264; DB 14; Length 1311;
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Best Local Similarity 82.8%; Pred. No. 6,8e-23;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy      1 YPVRCLLPATGPKARIRIRWYFVASVGQCNRFVYGGCGNANNFASBOECMSSCGGS 58
Db      732 YPVRCLLPASGSCADMARWTFVASVGQCNRFWYGCGHGNANNFASBOECMSSCGGS 789

RESULT 11
; US-10-391-364-91
; Sequence 91, Application US/10391364
; Publication No. US20040121349A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Cook, William James
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Welch, Nadine S.
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: NOVEL 27877, 18080, 14081, 32140, 50352,
; FILE REFERENCE: 16658, 14223, 16002, 50566, 65552 AND 65577 MOLECULES AND
; FILE REFERENCE: MP103-019QNMIM
; CURRENT APPLICATION NUMBER: US/10/391,364
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 09/950,370
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/231,084
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 10/294,039
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 60/338,587
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 10/266,035
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US 60/328,198
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/717,926
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 60/214,707
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 10/268,036
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/327,820
; PRIOR FILING DATE: 2001-10-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 1311
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-391-364-91

Query Match      80.2%; Score 264; DB 16; Length 1311;
Best Local Similarity 82.8%; Pred. No. 6,8e-23;
Matches 48; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy      1 YPVRCLLPATGPKARIRIRWYFVASVGQCNRFVYGGCGNANNFASBOECMSSCGGS 58
Db      722 YPVRCLLPASGSCADMARWTFVASVGQCNRFWYGCGHGNANNFASBOECMSSCGGS 789

RESULT 12
; US-10-087-887-86
; Sequence 86, Application US/10087887
; Publication No. US20030198957A1
; GENERAL INFORMATION:
; APPLICANT: Rekuda, Ramesh
; APPLICANT: Conley, Pamela B.
; APPLICANT: Yang, Ruy-Bing
; APPLICANT: Hart, Matthew
```



APPLICANT: Tomlinson, James E.  
 APPLICANT: Topper, James N.  
 APPLICANT: Shimkets, Richard A.  
 APPLICANT: Leach, Martin D.  
 APPLICANT: Zernhusen, Bryan D.  
 APPLICANT: Komuves, Laszlo  
 APPLICANT: Padigaru, Muralidhara  
 TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
 FILE REFERENCE: 21402-285  
 CURRENT APPLICATION NUMBER: US/10/087,887  
 CURRENT FILING DATE: 2002-03-01  
 PRIOR APPLICATION NUMBER: 60/273,049  
 PRIOR FILING DATE: 2001-03-02  
 PRIOR APPLICATION NUMBER: 60/279,883  
 PRIOR FILING DATE: 2001-03-29  
 PRIOR APPLICATION NUMBER: 60/277,791  
 PRIOR FILING DATE: 2001-03-21  
 PRIOR APPLICATION NUMBER: 60/281,248  
 PRIOR FILING DATE: 2001-04-03  
 PRIOR APPLICATION NUMBER: 60/282,864  
 PRIOR FILING DATE: 2001-04-10  
 PRIOR APPLICATION NUMBER: 60/282,537  
 PRIOR FILING DATE: 2001-04-09  
 PRIOR APPLICATION NUMBER: 60/282,867  
 PRIOR FILING DATE: 2001-04-10  
 NUMBER OF SEQ ID NOS: 104  
 SOFTWARE: Cuiaseq1 version 0.1  
 SEQ ID NO: 86  
 LENGTH: 1280  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-10-087-887-86

Query Match 74.8%; Score 246; DB 14; Length 1280;  
 Best Local Similarity 75.4%; Pred. No. 9,8e-21;  
 Matches 43; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 YPVRCLIPATGPKARIIRMYFVAVGQCNRFYGGCGRGNANFASQECMSSCOG 57  
 Db 746 YPVRCLIPASAGSGCDWAAWYFVAVGRCNRFYGGCGHANNFASQECMTCRG 802

RESULT 13  
 US-08-896-322-5  
 Sequence 5, Application US/08896322  
 Publication No. US20020103334A1  
 GENERAL INFORMATION:  
 APPLICANT: Werner Schroeder, Soren Bjorn, Kjeld No. US20020103334A1,ris, Viggo Dinesen  
 TITLE OF INVENTION: APROTININ VARIANTS HAVING IMPROVED PRO  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SPRUNG KRAMER SCHAEFER & BRISCOE  
 STREET: 660 White Plains Road  
 City: Tarrytown  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10591-5144  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage  
 COMPUTER: HP VECTRA  
 OPERATING SYSTEM: DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/896,322  
 FILING DATE: 17-JUL-1997  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 196 29 982.9 (Germany)  
 FILING DATE: 25-JUL-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kurt G. Briscoe  
 REGISTRATION NUMBER: 33,141  
 REFERENCE/DOCKET NUMBER: Bayer 9911-KGB

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (914) 332-1700  
 TELEFAX: (914) 332-1844  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 57 amino acids  
 TYPE: Amino acid  
 STRANDEDNESS: Single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 FRAGMENT TYPE: linear  
 ORIGINAL SOURCE:  
 ORGANISM: Aprotinin variant  
 US-08-896-322-5

Query Match 58.7%; Score 193; DB 8; Length 57;  
 Best Local Similarity 57.4%; Pred. No. 1.2e-15;  
 Matches 31; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 5 CLAPPATGPKARIIRMYFVAVGQCNRFYGGCGRGNANFASQECMSSCOG 58  
 Db 4 CLPPTGPKRAIIRYFDATAGLCTTFYGGCRANRNFKSAEDCMETCGA 57

RESULT 14  
 US-10-252-967-5  
 Sequence 5, Application US/10252967  
 Publication No. US20030096752A1  
 GENERAL INFORMATION:  
 APPLICANT: Werner Schroeder, Soren Bjorn, Kjeld No. US20030096752A1,ris, Viggo Dine  
 TITLE OF INVENTION: APROTININ VARIANTS HAVING IMPROVED PRO  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SPRUNG KRAMER SCHAEFER & BRISCOE  
 STREET: 660 White Plains Road  
 City: Tarrytown  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10591-5144  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage  
 COMPUTER: HP VECTRA  
 OPERATING SYSTEM: DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/252,967  
 FILING DATE: 23-Sep-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/896,322  
 FILING DATE: 17-JUL-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kurt G. Briscoe  
 REGISTRATION NUMBER: 33,141  
 REFERENCE/DOCKET NUMBER: Bayer 9911-KGB  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (914) 332-1700  
 TELEFAX: (914) 332-1844  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 57 amino acids  
 TYPE: Amino acid  
 STRANDEDNESS: Single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 FRAGMENT TYPE: linear  
 ORIGINAL SOURCE:  
 ORGANISM: Aprotinin variant  
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 US-10-252-967-5

Query Match 58.7%; Score 193; DB 14; Length 57;  
Best Local Similarity 57.4%; Pred. No. 1.2e-15;  
Matches 31; Conservative 10; Mismatches 13; Indels 0; Gaps 0;  
QY 5 CLLPATGPKARIIRMYFVASVGGCNRFPYGGCRGNANFPASQECMSSCGS 58  
DB 4 CLFPSTGPKARIIRFYDATAGLCETFYGGCRANRNFKSAEDCMETCGA 57

## RESULT 15

US-09-234-874A-7  
; Sequence 7, Application US/09234874A  
; Publication NO. US2001002003A1  
; GENERAL INFORMATION:  
; APPLICANT: White, Tyler R.  
; Lesikar, David D.  
; Damm, Deborah  
; McFadden, Kathleen  
; Garrick, Brett L.  
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES  
; NUMBER OF SEQUENCES: 228  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/234,874A  
; FILING DATE: 11-Jun-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/436,555  
; FILING DATE: 08-MAY-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 056324/0106  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 58 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-234-874A-7

Query Match 58.4%; Score 192; DB 9; Length 58;  
Best Local Similarity 57.9%; Pred. No. 1.7e-15;  
Matches 33; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 2 PYRCLLPATGPKARIIRMYFVASVGGCNRFPYGGCRGNANFPASQECMSSCGS 58  
DB 2 PDFCLPFPYTGPKARIIRFYNAKAGLCQTFYGGCRANRNFKSAEDCMRTCGA 58

Search completed: August 25, 2005, 04:59:08  
Job time : 164 secs

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